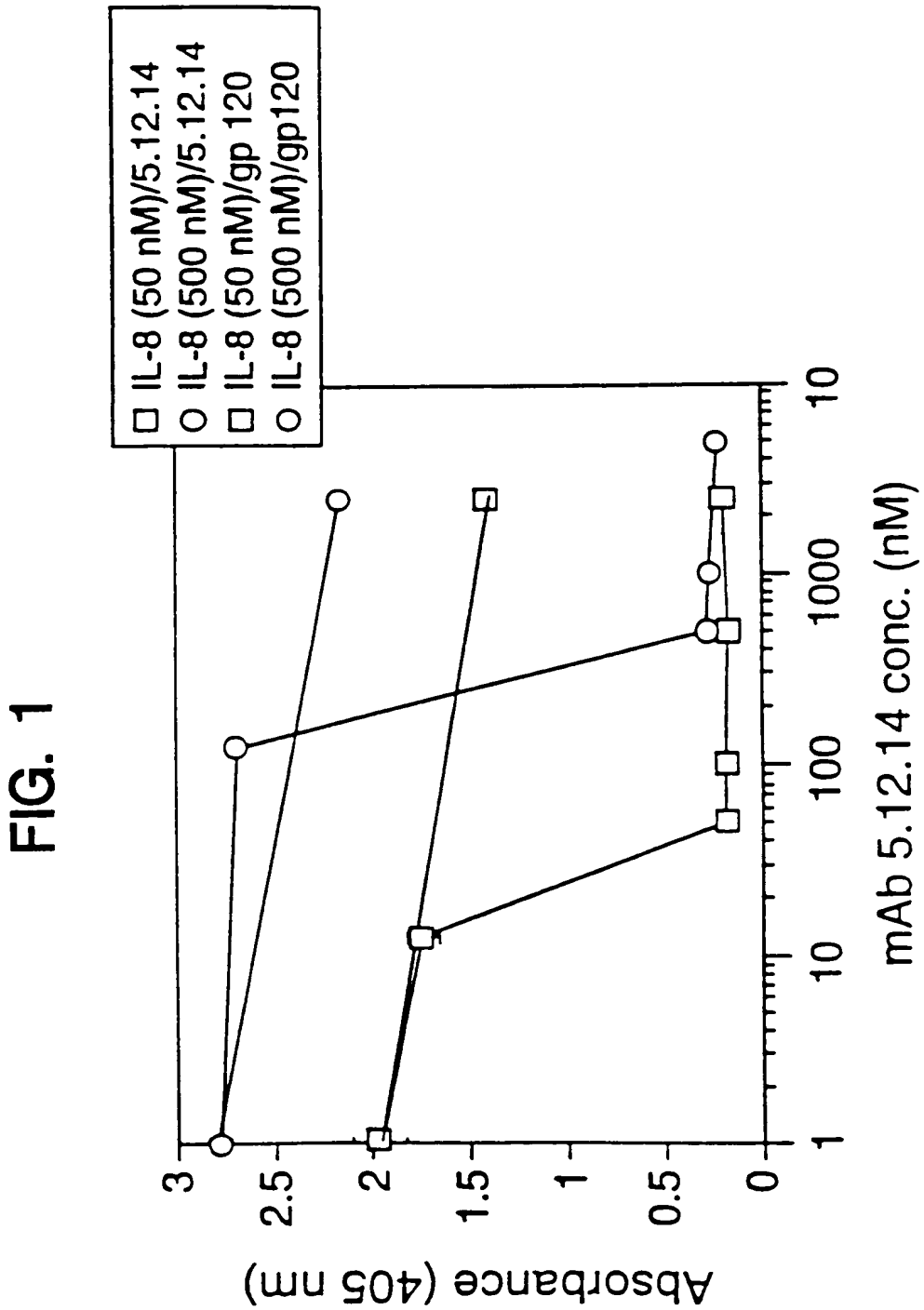
FIG. 1



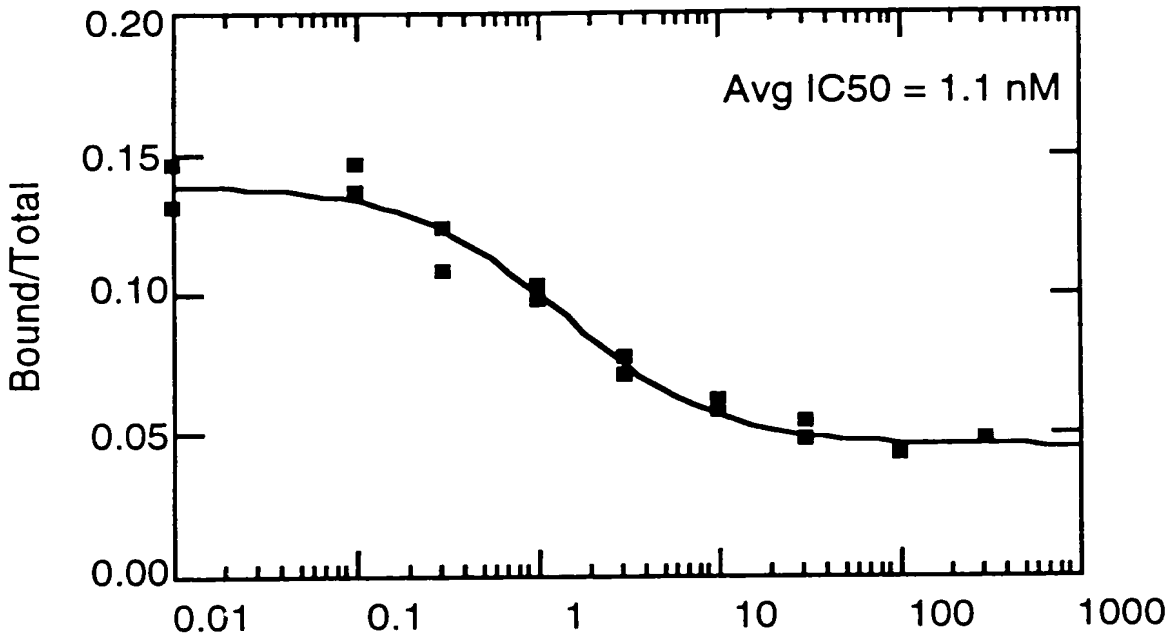


FIG. 2

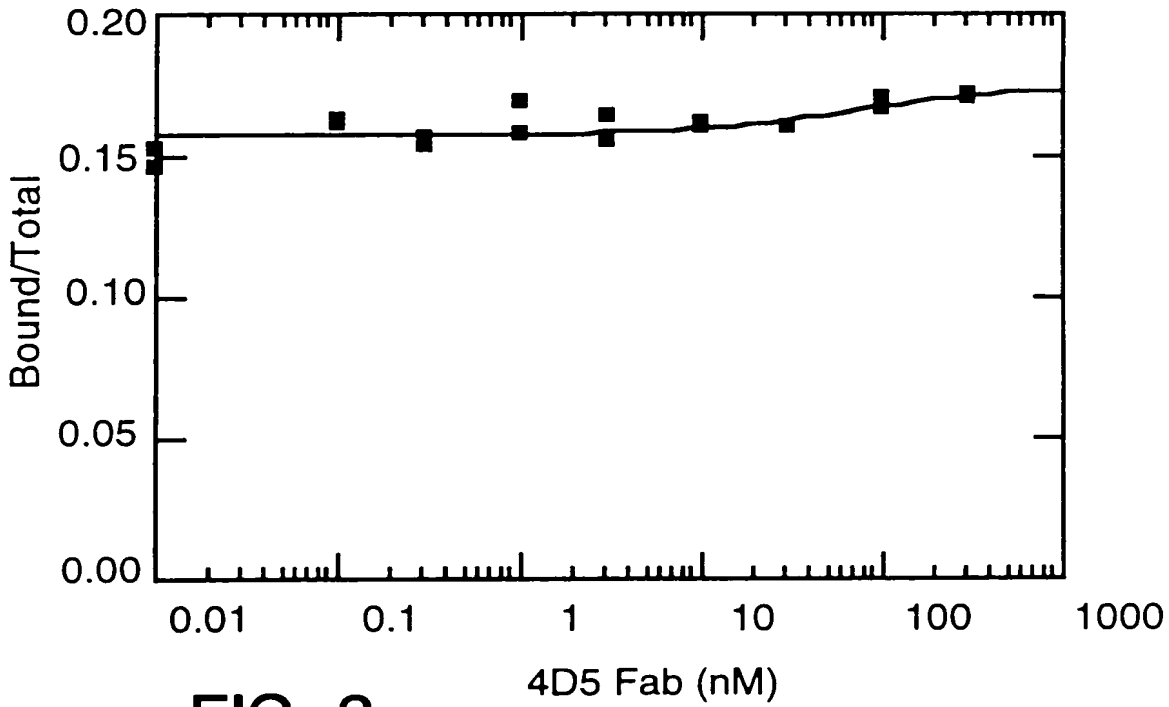


FIG. 3

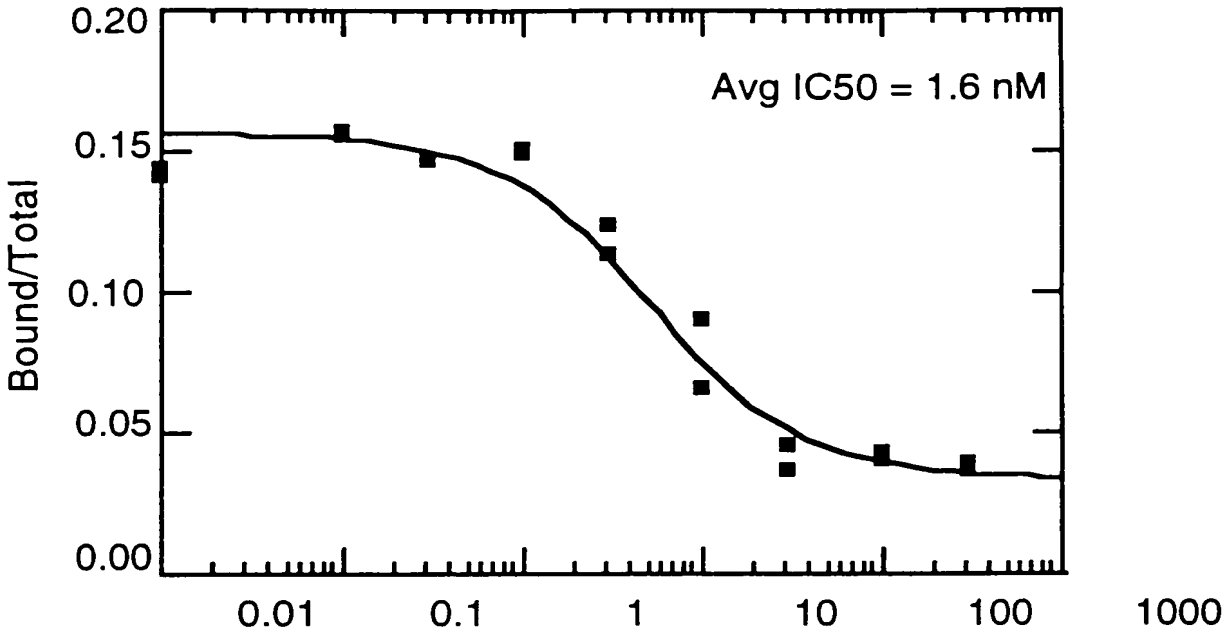


FIG. 4

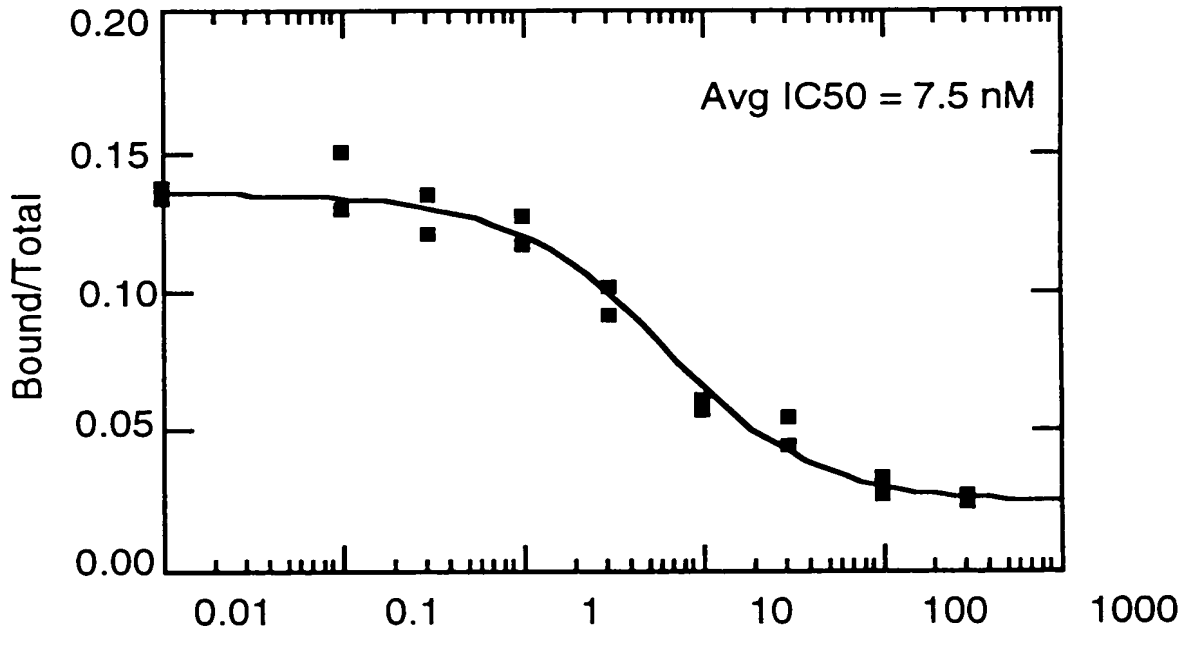


FIG. 5

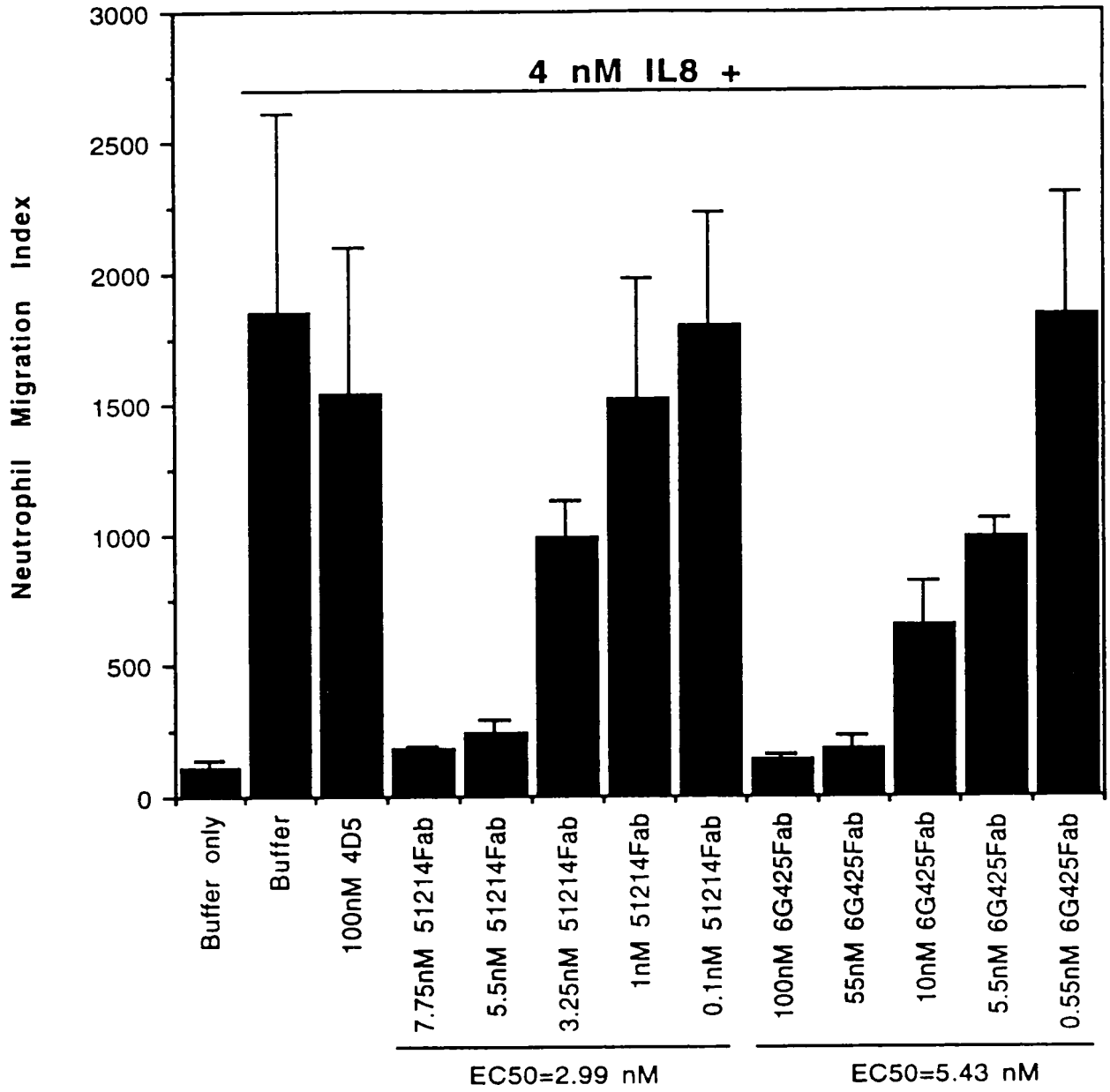


FIG. 6

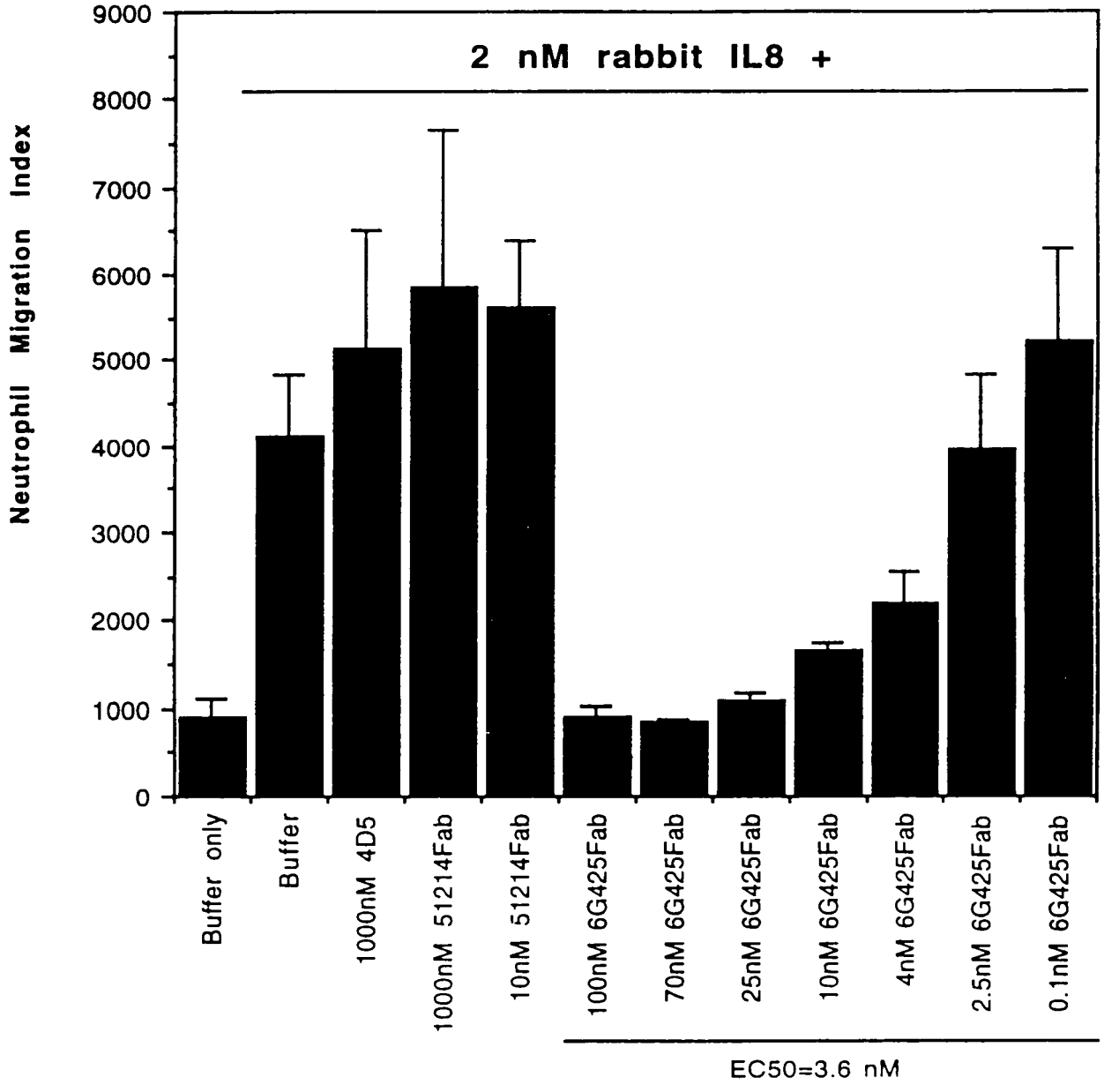


FIG. 7

FIG. 8

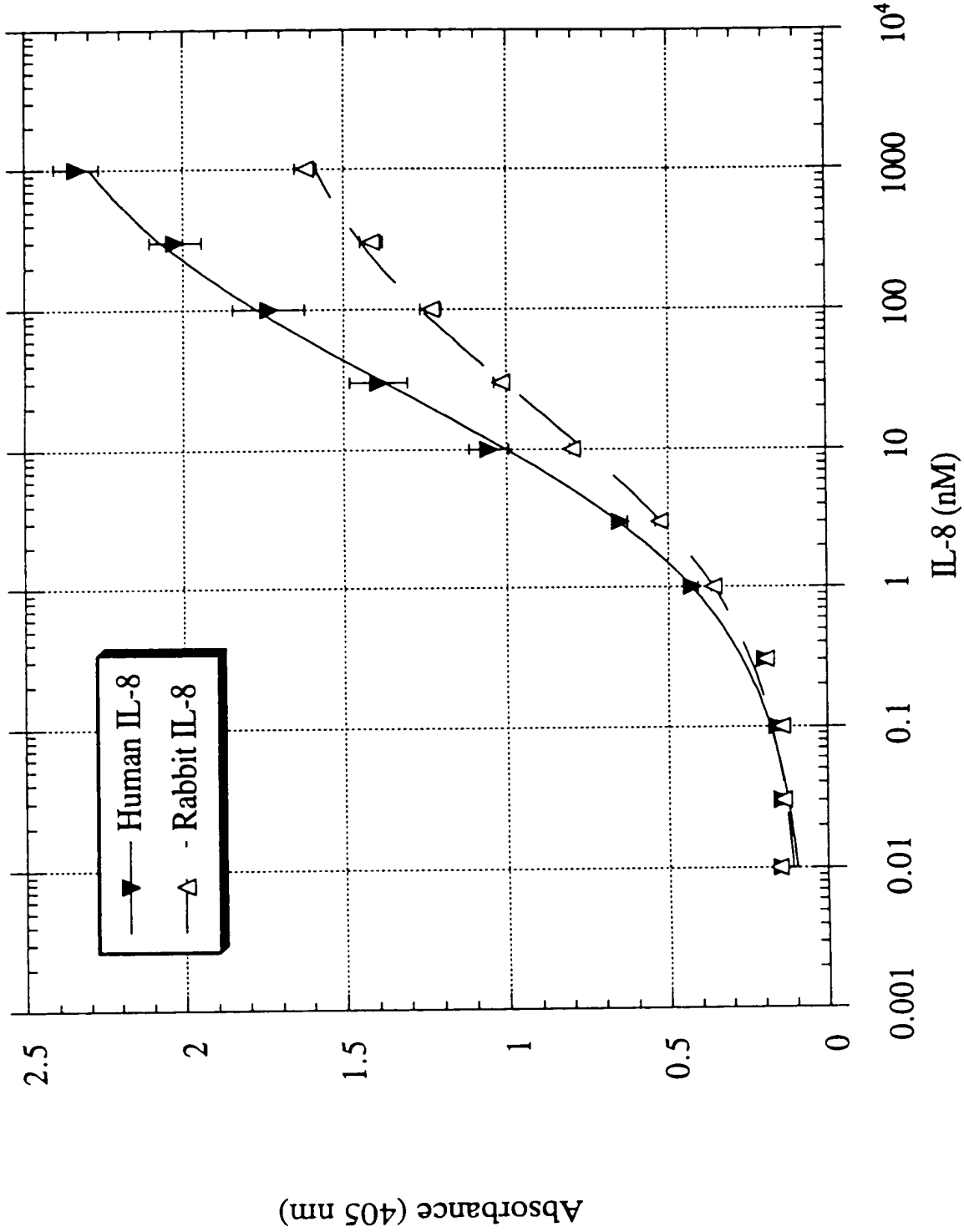


FIG. 9

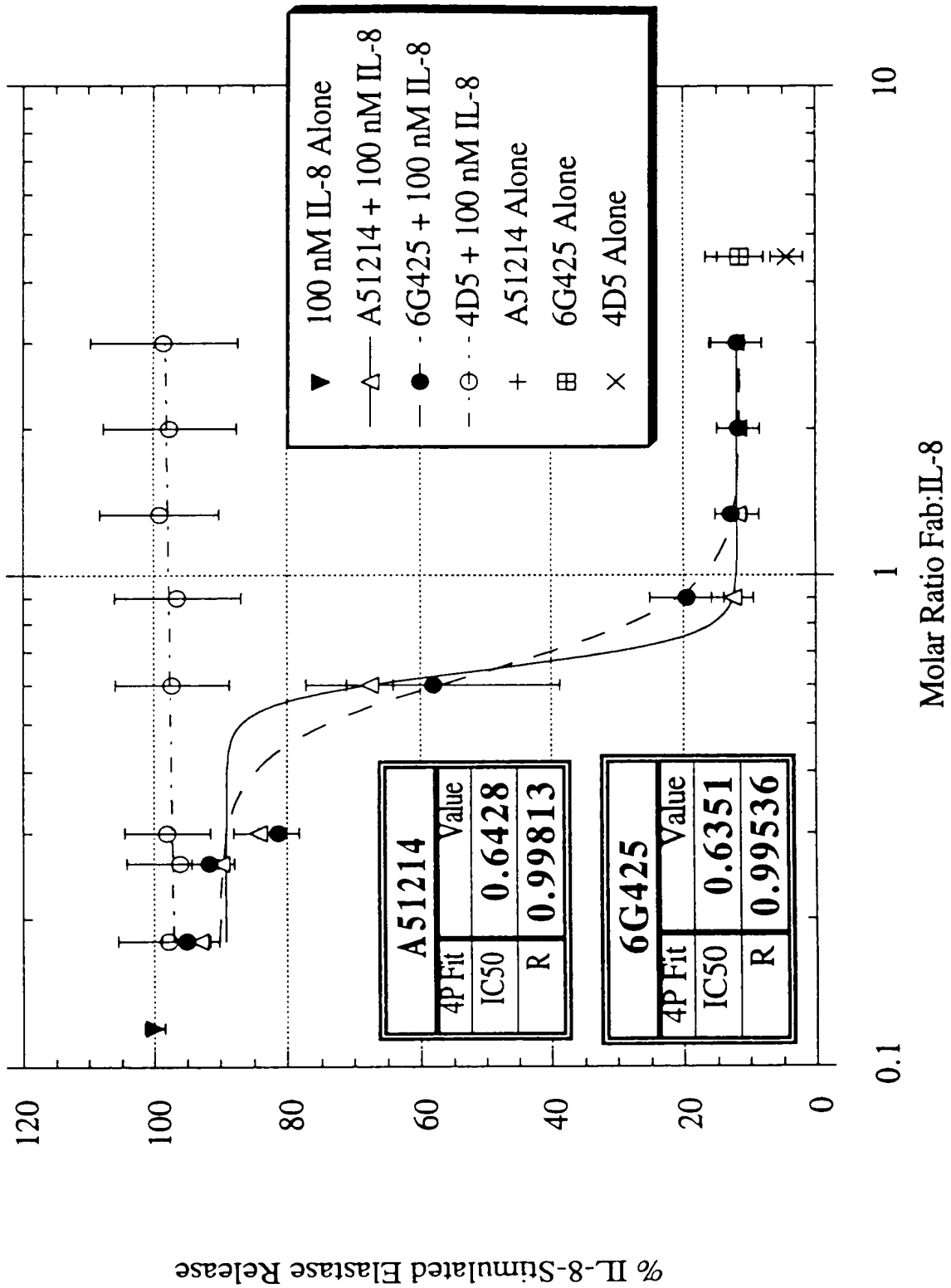
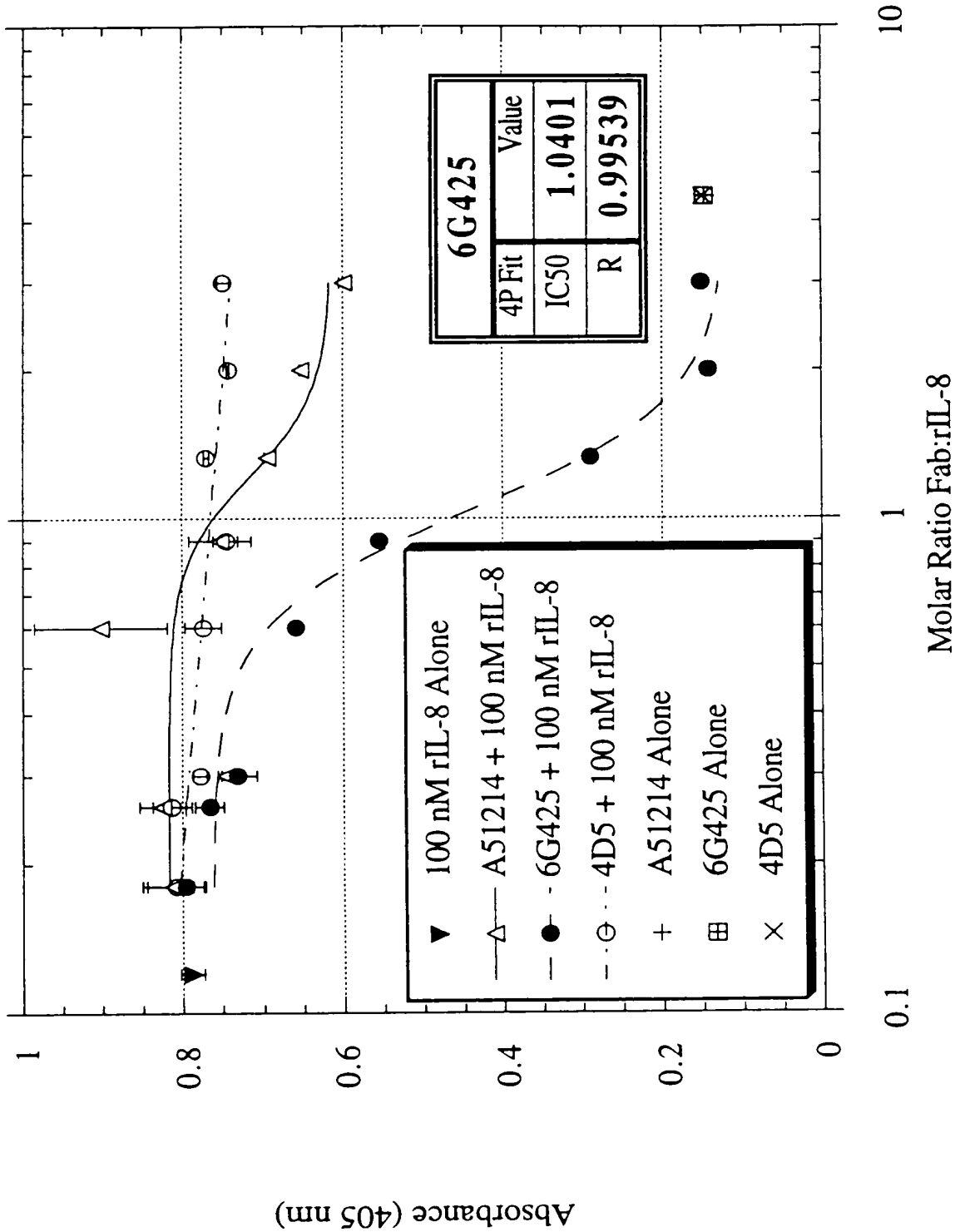


FIG. 10



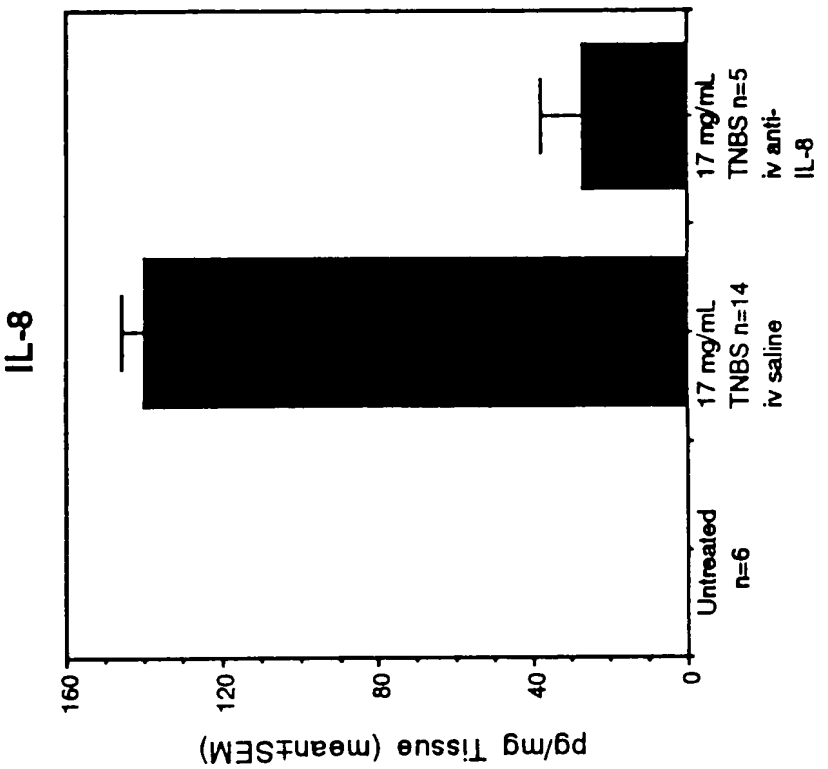


FIG. 11B

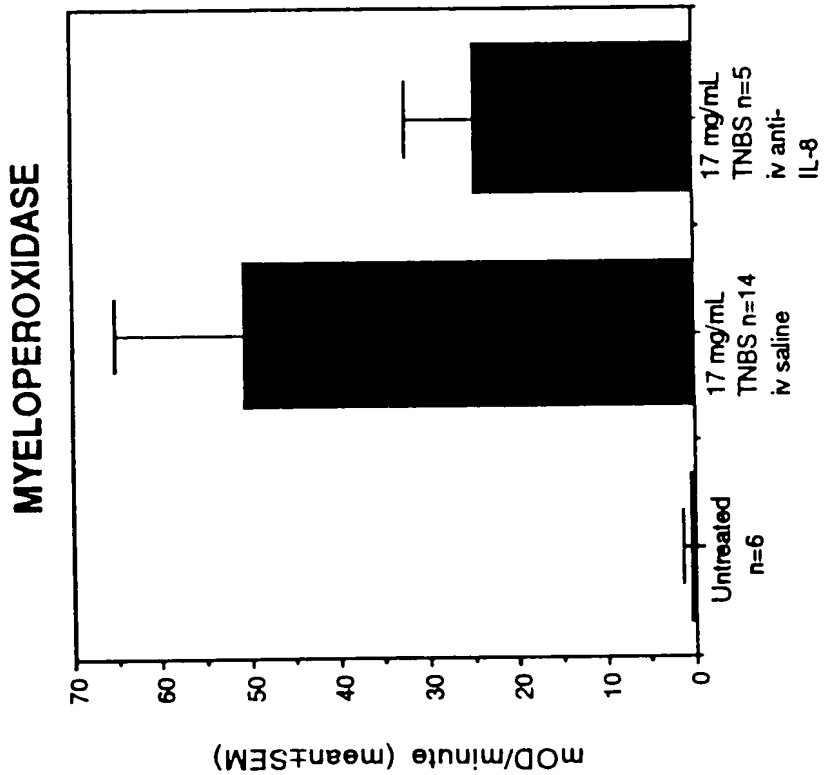


FIG. 11A

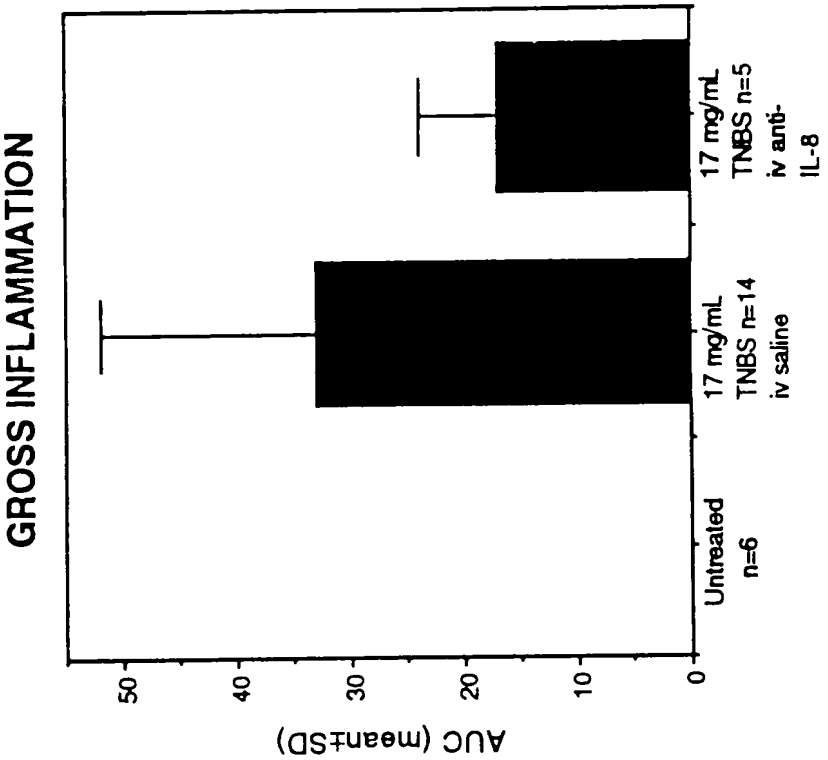


FIG. 11D

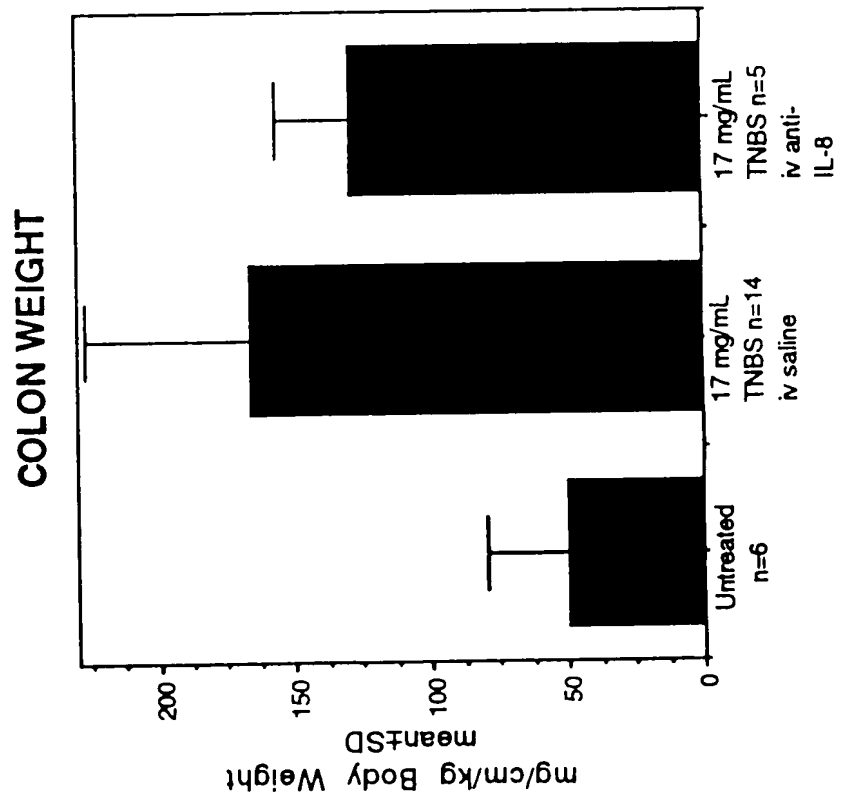


FIG. 11C

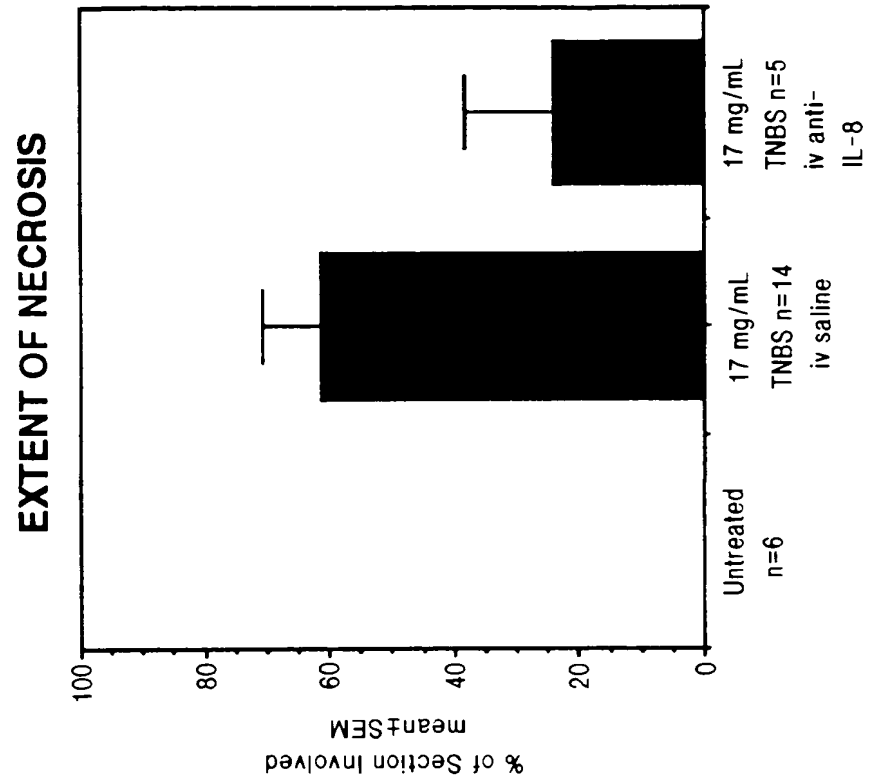


FIG. 11F

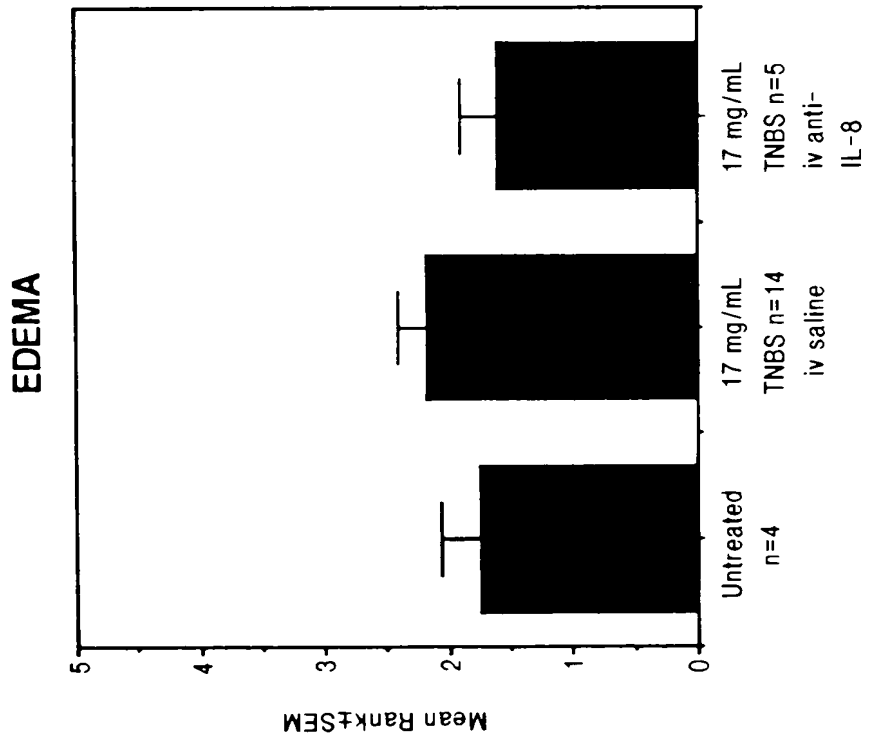


FIG. 11E

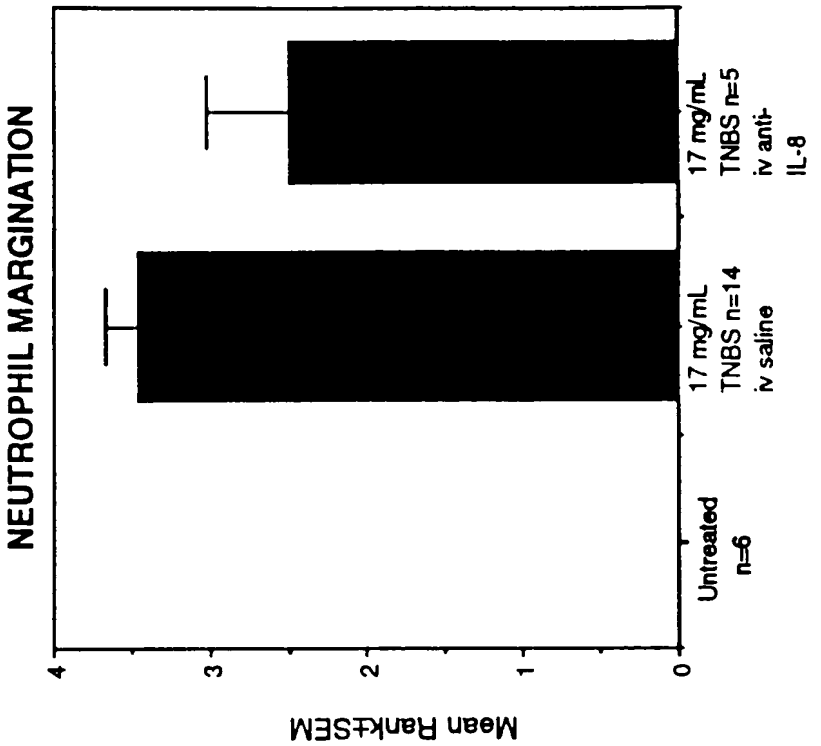


FIG. 11H

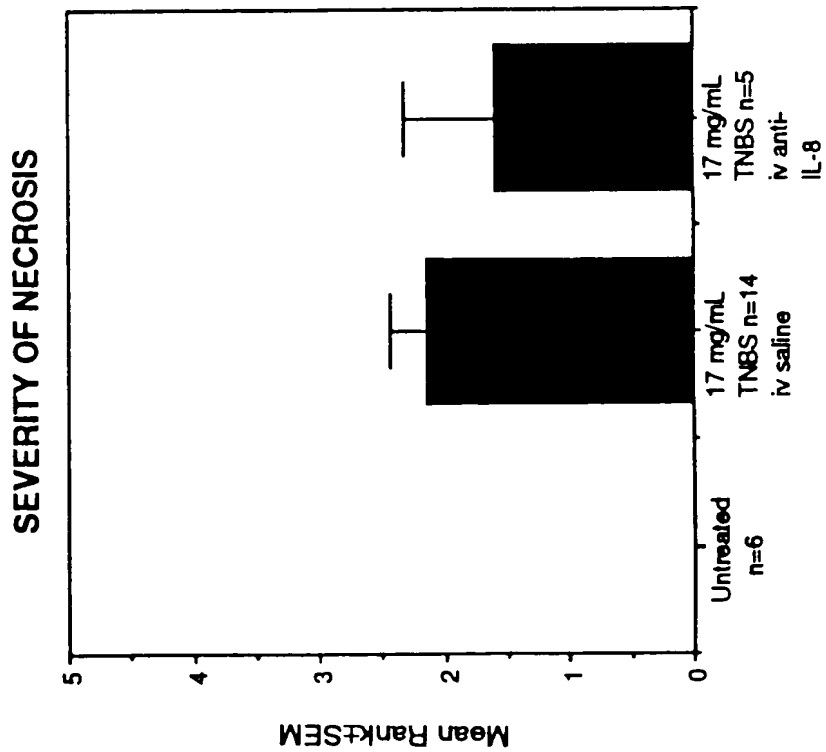


FIG. 11G

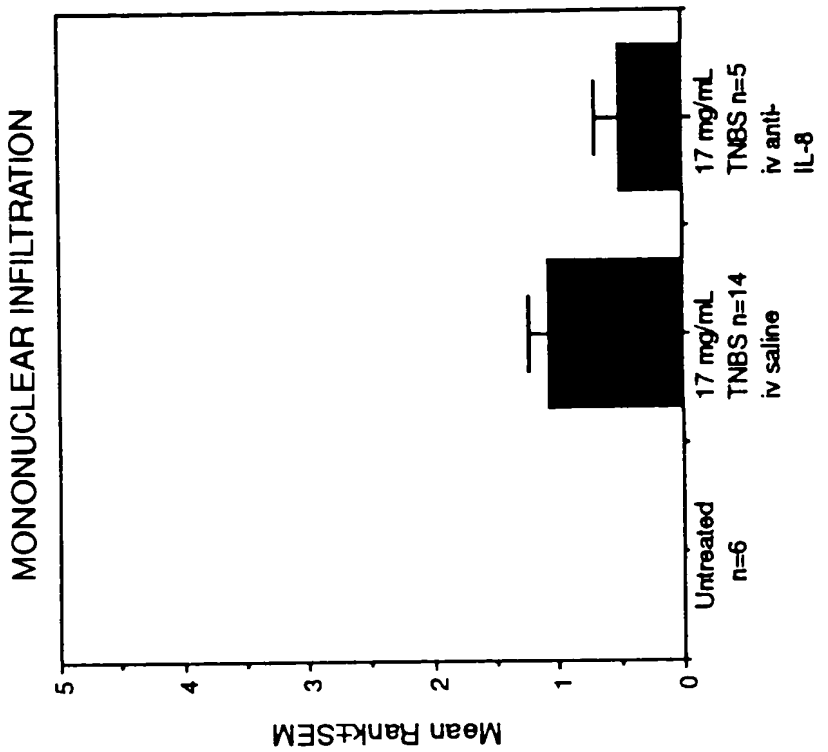


FIG. 11J

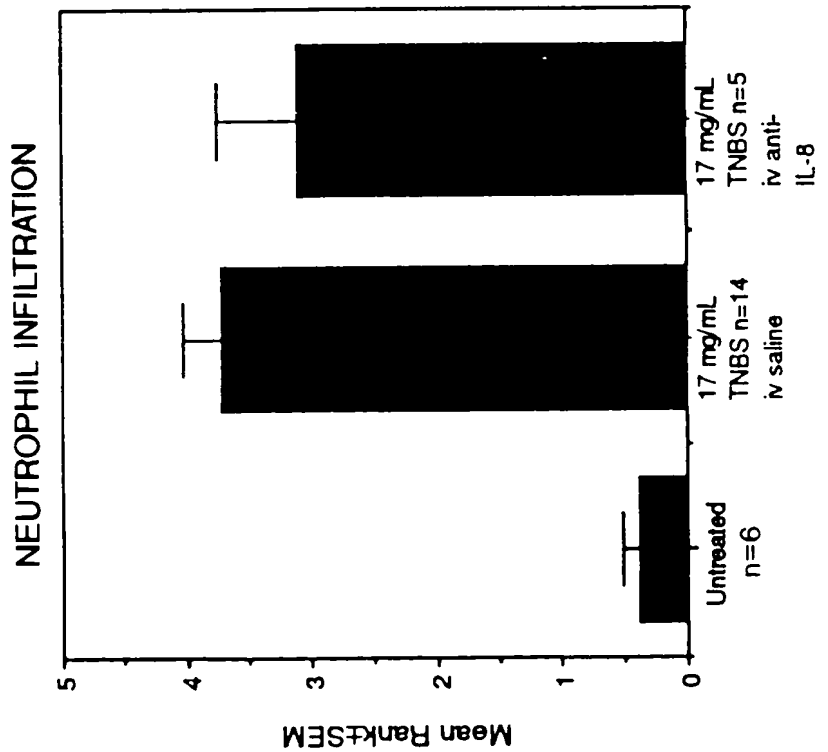


FIG. 11I

FIG. 12

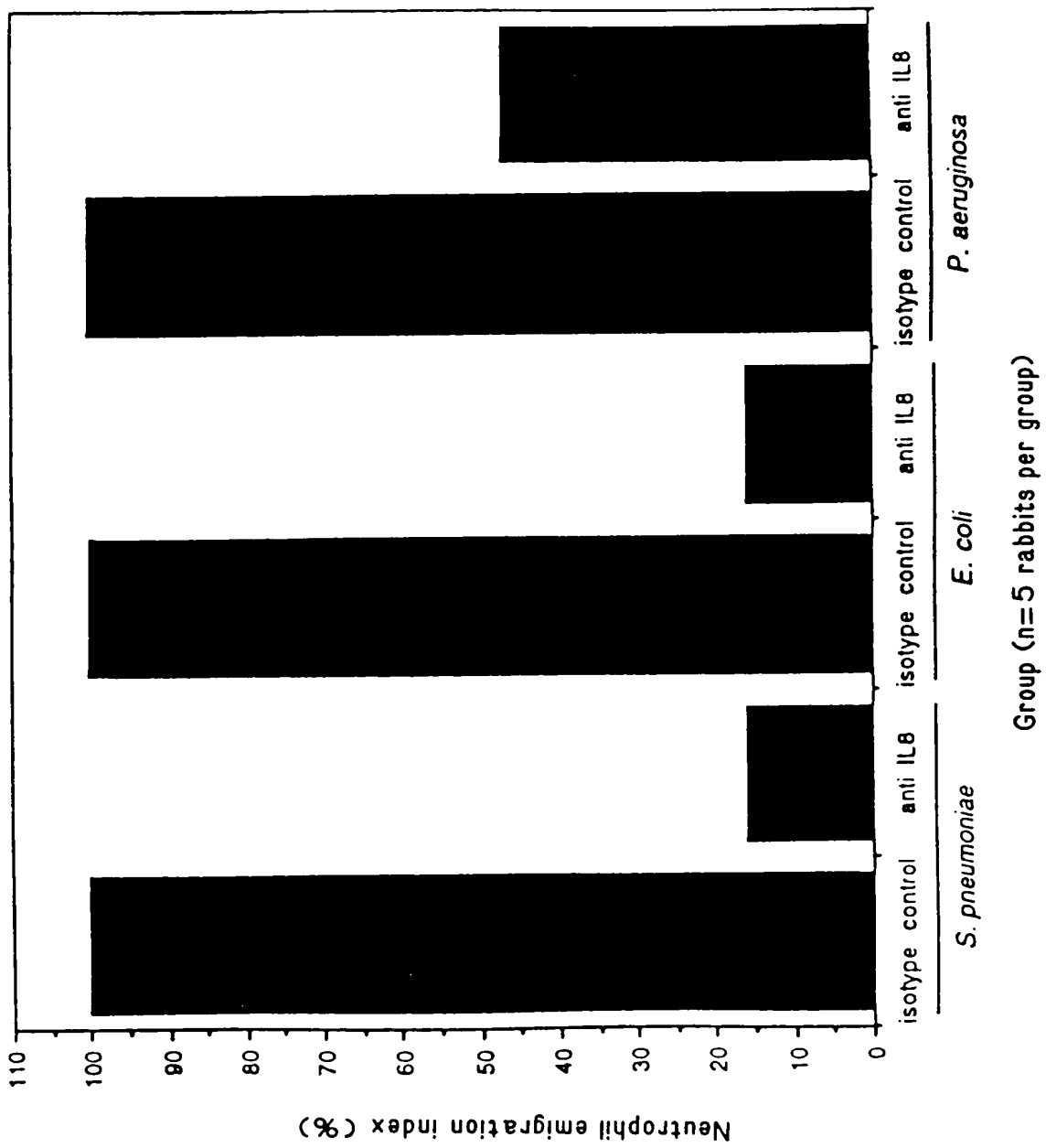


FIG. 13

Light Chain Primers:

MKLC-1, 22mer

5' CAGTCCAACTGTTCAGGACGCC 3' (SEQ ID NO.1)

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3' (SEQ ID NO.2)

MKLC-3, 23mer

5' GAAGTTGATGTCTTGTGAGTGGC 3' (SEQ ID NO.3)

Heavy Chain Primers:

IGG2AC-1, 24mer

5' GCATCCTAGAGTCACCGAGGAGCC 3' (SEQ ID NO.4)

IGG2AC-2, 22mer

5' CACTGGCTCAGGGAAATAACCC 3' (SEQ ID NO.5)

IGG2AC-3, 22mer

5' GGAGAGCTGGGAAGGTGTGCAC 3' (SEQ ID NO.6)

FIG. 14

Light chain forward primer

SL001A-2 35 mer

5' ACAAACGCGTACGCT GACATCGTCATGACCCAGTC 3' (SEQ ID NO.7)
T T T (SEQ ID NO.8)
A (SEQ ID NO.9)

Light chain reverse primer

SL001B 37 mer

5' GCTCTTCGAATG GTGGGAAGATGGATACAGTTGGTGC 3' (SEQ ID NO.10)

Heavy chain forward primer

SL002B 39 mer

5' CGATGGGCCCGG ATAGACCGATGGGGCTGTTGTTTTGGC 3' (SEQ ID NO.11)
T C (SEQ ID NO.12)
G (SEQ ID NO.13)
A (SEQ ID NO.14)

FIG. 15

Heavy chain reverse primer

SL002B 39-MER

5' CGATGGGCCCGG ATAGACCGATGGGGCTGTTGTTTTGGC 3' (SEQ ID NO.11)
T (SEQ ID NO.15)
A (SEQ ID NO.14)
G (SEQ ID NO.13)

```
  1 GACATTGTCA TGACACAGTC TCAAAAATTC ATGTCCACAT CAGTAGGAGA CAGGGTCAGC
    CTGTAACAGT ACTGTGTCAG AGTTTTTAAG TACAGGTGTA GTCATCCTCT GTCCCAGTCG
  1 D  I  V  M   T  Q  S   Q  K  F   M  S  T  S   V  G  D   R  V  S

 61 GTCACCTGCA AGGCCAGTCA GAATGTGGGT ACTAATGTAG CCTGGTATCA ACAGAAACCA
    CAGTGGACGT TCCGGTCAGT CTTACACCCA TGATTACATC GGACCATAGT TGTCTTTGGT
 21 V  T  C  K   A  S  Q  N  V  G   T  N  V  A   W  Y  Q   Q  K  P
               *   *  *  *  *  *  *   *  *  *  *
                                CDR #1

121 GGGCAATCTC CTAAAGCACT GATTTACTCG TCATCCTACC GGTACAGTGG AGTCCCTGAT
    CCCGTTAGAG GATTTCGTGA CTAAATGAGC AGTAGGATGG CCATGTCACC TCAGGGACTA
 41 G  Q  S  P   K  A  L   I  Y  S   S  S  Y  R   Y  S  G   V  P  D
                                  *   *  *  *  *   *  *
                                          CDR #2

181 CGCTTCACAG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCCA TGTGCAGTCT
    GCGAAGTGTC CGTCACCTAG ACCCTGTCTA AAGTGAGAGT GGTAGTCGGT ACACGTCAGA
 61 R  F  T  G   S  G  S   G  T  D   F  T  L  T   I  S  H   V  Q  S

241 GAAGACTTGG CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCT
    CTTCTGAACC GTCTGATAAA GACAGTCGTT ATATTGTAGA TAGGAGAGTG CAAGCCAGGA
 81 E  D  L  A   D  Y  F   C  Q  Q   Y  N  I  Y   P  L  T   F  G  P
                              *  *   *  *  *  *   *  *  *
                                     CDR #3

301 GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC CATCTTCCCA
    CCCTGGTTCG ACCTCAACTT TGCCCGACTA CGACGTGGTG GTTGACATAG GTAGAAGGGT
101 G  T  K  L   E  L  K   R  A  D   A  A  P  P   T  V  S   I  F  P

       BstBI
361 CCATTCGAA (SEQ ID NO.16)
    GGTAAGCTT
121 P  F  E   (SEQ ID NO.17)
```

FIG. 16

```
  1 TTCTATTGCT ACAAACGCGT ACGCTGAGGT GCAGCTGGTG GAGTCTGGGG GAGGCTTAGT
    AAGATAACGA TGTTTGCGCA TGCGACTCCA CGTCGACCAC CTCAGACCCC CTCCGAATCA
  1                             E  V   Q  L  V   E  S  G  G   G  L  V

 61 GCCGCCTGGA GGGTCCCTGA AACTCTCCTG TGCAGCCTCT GGATTCATAT TCAGTAGTTA
    CGGCGGACCT CCCAGGGACT TTGAGAGGAC ACGTCGGAGA CCTAAGTATA AGTCATCAAT
 13  P  P  G   G  S  L  K   L  S  C   A  A  S   G  F  I  F   S  S  Y
                                                              *  *

                                                        CDR #1

121 TGGCATGTCT TGGGTTCGCC AGACTCCAGG CAAGAGCCTG GAGTTGGTCG CAACCATTAA
    ACCGTACAGA ACCCAAGCGG TCTGAGGTCC GTTCTCGGAC CTCAACCAGC GTTGGTAATT
 33  G  M  S   W  V  R  Q   T  P  G   K  S  L   E  L  V  A   T  I  N
     *  *  *                                                 *  *  *

181 TAATAATGGT GATAGCACCT ATTATCCAGA CAGTGTGAAG GGCCGATTCA CCATCTCCCG
    ATTATTACCA CTATCGTGGA TAATAGGTCT GTCACACTTC CCGGCTAAGT GGTAGAGGGC
 53  N  N  G   D  S  T  Y   Y  P  D   S  V  K   G  R  F  T   I  S  R
     *  *  *   *  *  *  *   *  *  *   *  *  *

                      CDR #2

241 AGACAATGCC AAGAACACCC TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC
    TCTGTTACGG TTCTTGTGGG ACATGGACGT TTACTCGTCA GACTTCAGAC TCCTGTGTCG
 73  D  N  A   K  N  T  L   Y  L  Q   M  S  S   L  K  S  E   D  T  A

301 CATGTTTTAC TGTGCAAGAG CCCTCATTAG TTCGGCTACT TGGTTTGGTT ACTGGGGCCA
    GTACAAAATG ACACGTTCTC GGGAGTAATC AAGCCGATGA ACCAAACCAA TGACCCCGGT
 93  M  F  Y   C  A  R  A   L  I  S   S  A  T   W  F  G   Y   W  G  Q
                    *      *  *  *   *  *  *   *  *  *   *

                                CDR #3

361 AGGGACTCTG GTCACTGTCT CTGCAGCCAA AACAACAGCC CCATCTGTCT
    TCCCTGAGAC CAGTGACAGA GACGTCGGTT TTGTTGTCGG GGTAGACAGA
113  G  T  L   V  T  V  S   A  A  K   T  T  A   P  S  V  Y

        ApaI
411   ATCCGGG  (SEQ ID NO.18)
      TAGGCCC
130     P      (SEQ ID NO.19)
```

FIG. 17

FIG. 18

VL.front 31-MER

5' ACAAACGCGTACGCTGATATCGTCATGACAG 3' (SEQ ID NO.20)

VL.rear 31-MER

5' GCAGCATCAGCTCTTCGAAGCTCCAGCTTGG 3' (SEQ ID NO.21)

VH.front.SPE 21-MER

5' CCACTAGTACGCAAGTTCACG 3' (SEQ ID NO.22)

VH.rear 33-MER

5' GATGGGCCCTTGGTGGAGGCTGCAGAGACAGTG 3' (SEQ ID NO.23)

```
   1 ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC
     TACTTCTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23  M  K  K  N    I  A  F    L  L  A    S  M  F  V    F  S  I    A  T  N

  61 GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA TGTCCACATC AGTAGGAGAC
     CGCATGCGAC TATAGCAGTA CTGTGTCAGA GTTTTTAAGT ACAGGTGTAG TCATCCTCTG
 -3  A  Y  A  D    I  V  M    T  Q  S    Q  K  F  M    S  T  S    V  G  D

 121 AGGGTCAGCG TCACCTGCAA GGCCAGTCAG AATGTGGGTA CTAATGTAGC CTGGTATCAA
     TCCCAGTCGC AGTGGACGTT CCGGTCAGTC TTACACCCAT GATTACATCG GACCATAGTT
  18  R  V  S  V    T  C  K    A  S  Q    N  V  G  T    N  V  A    W  Y  Q
                          *    *  *  *    *  *  *  *    *  *  *
                                                 CDR #1

 181 CAGAAACCAG GGCAATCTCC TAAAGCACTG ATTTACTCGT CATCCTACCG GTACAGTGGA
     GTCTTTGGTC CCGTTAGAGG ATTTCGTGAC TAAATGAGCA GTAGGATGGC CATGTCACCT
  38  Q  K  P  G    Q  S  P    K  A  L    I  Y  S  S    S  Y  R    Y  S  G
                                          *  *  *  *    *  *  *
                                                 CDR #2

 241 GTCCCTGATC GCTTCACAGG CAGTGGATCT GGGACAGATT TCACTCTCAC CATCAGCCAT
     CAGGGACTAG CGAAGTGTCC GTCACCTAGA CCCTGTCTAA AGTGAGAGTG GTAGTCGGTA
  58  V  P  D  R    F  T  G    S  G  S    G  T  D  F    T  L  T    I  S  H

 301 GTGCAGTCTG AAGACTTGGC AGACTATTTC TGTCAGCAAT ATAACATCTA TCCTCTCACG
     CACGTCAGAC TTCTGAACCG TCTGATAAAG ACAGTCGTTA TATTGTAGAT AGGAGAGTGC
  78  V  Q  S  E    D  L  A    D  Y  F    C  Q  Q  Y    N  I  Y    P  L  T
                                          *  *  *  *    *  *  *    *  *  *
                                                 CDR #3

                                      BstBI
 361 TTCGGTCCTG GGACCAAGCT GGAGCTTCGA AGAGCTGTGG CTGCACCATC TGTCTTCATC
     AAGCCAGGAC CCTGGTTCGA CCTCGAAGCT TCTCGACACC GACGTGGTAG ACAGAAGTAG
  98  F  G  P  G    T  K  L    E  L  R    R  A  V  A    A  P  S    V  F  I

 421 TTCCCGCCAT CTGATGAGCA GTTGAAATCT GGAACTGCTT CTGTTGTGTG CCTGCTGAAT
     AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGAA GACAACACAC GGACGACTTA
 118  F  P  P  S    D  E  Q    L  K  S    G  T  A  S    V  V  C    L  L  N

 481 AACTTCTATC CCAGAGAGGC CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT
     TTGAAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA
 138  N  F  Y  P    R  E  A    K  V  Q    W  K  V  D    N  A  L    Q  S  G

 541 AACTCCCAGG AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
     TTGAGGGTCC TCTCACAGTG TCTCGTCCTG TCGTTCCTGT CGTGGATGTC GGAGTCGTCG
 158  N  S  Q  E    S  V  T    E  Q  D    S  K  D  S    T  Y  S    L  S  S

 601 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC
     TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG
 178  T  L  T  L    S  K  A    D  Y  E    K  H  K  V    Y  A  C    E  V  T

 661 CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA GGGGAGAGTG
     GTAGTCCCGG ACTCGAGCGG GCAGTGTTTC TCGAAGTTGT CCCCTCTCAC
 198  H  Q  G  L    S  S  P    V  T  K    S  F  N  R    G  E  C  (SEQ ID NO.25)

 711    TTAA  (SEQ ID NO.24)
        AATT
 216     O
```

FIG. 19

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N

 61 GCGTACGCTG AGGTGCAGCT GGTGGAGTCT GGGGGAGGCT TAGTGCCGCC TGGAGGGTCC
    CGCATGCGAC TCCACGTCGA CCACCTCAGA CCCCCTCCGA ATCACGGCGG ACCTCCCAGG
 -3 A  Y  A  E  V  Q  L  V  E  S  G  G  G  L  V  P  P  G  G  S

121 CTGAAACTCT CCTGTGCAGC CTCTGGATTC ATATTCAGTA GTTATGGCAT GTCTTGGGTT
    GACTTTGAGA GGACACGTCG GAGACCTAAG TATAAGTCAT CAATACCGTA CAGAACCCAA
 18 L  K  L  S  C  A  A  S  G  F  I  F  S  S  Y  G  M  S  W  V
                                             *  *  *  *  *
                                    CDR #1

181 CGCCAGACTC CAGGCAAGAG CCTGGAGTTG GTCGCAACCA TTAATAATAA TGGTGATAGC
    GCGGTCTGAG GTCCGTTCTC GGACCTCAAC CAGCGTTGGT AATTATTATT ACCACTATCG
 38 R  Q  T  P  G  K  S  L  E  L  V  A  T  I  N  N  N  G  D  S
                                          *  *  *  *  *  *  *  *

241 ACCTATTATC CAGACAGTGT GAAGGGCCGA TTCACCATCT CCCGAGACAA TGCCAAGAAC
    TGGATAATAG GTCTGTCACA CTTCCCGGCT AAGTGGTAGA GGGCTCTGTT ACGGTTCTTG
 58 T  Y  Y  P  D  S  V  K  G  R  F  T  I  S  R  D  N  A  K  N
    *  *  *  *  *  *  *  *
       CDR #2

301 ACCCTGTACC TGCAAATGAG CAGTCTGAAG TCTGAGGACA CAGCCATGTT TTACTGTGCA
    TGGGACATGG ACGTTTACTC GTCAGACTTC AGACTCCTGT GTCGGTACAA AATGACACGT
 78 T  L  Y  L  Q  M  S  S  L  K  S  E  D  T  A  M  F  Y  C  A

361 AGAGCCCTCA TTAGTTCGGC TACTTGGTTT GGTTACTGGG GCCAAGGGAC TCTGGTCACT
    TCTCGGGAGT AATCAAGCCG ATGAACCAAA CCAATGACCC CGGTTCCCTG AGACCAGTGA
 98 R  A  L  I  S  S  A  T  W  F  G  Y  W  G  Q  G  T  L  V  T
       *  *  *  *  *  *  *  *  *  *  *
                CDR #3
                      ApaI
421 GTCTCTGCAG CCTCCACCAA GGGCCCATCG GTCTTCCCCC TGGCACCCTC CTCCAAGAGC
    CAGAGACGTC GGAGGTGGTT CCCGGGTAGC CAGAAGGGGG ACCGTGGGAG GAGGTTCTCG
118 V  S  A  A  S  T  K  G  P  S  V  F  P  L  A  P  S  S  K  S

481 ACCTCTGGGG GCACAGCGGC CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG
    TGGAGACCCC CGTGTCGCCG GGACCCGACG GACCAGTTCC TGATGAAGGG GCTTGGCCAC
138 T  S  G  G  T  A  A  L  G  C  L  V  K  D  Y  F  P  E  P  V

541 ACGGTGTCGT GGAACTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA
    TGCCACAGCA CCTTGAGTCC GCGGGACTGG TCGCCGCACG TGTGGAAGGG CCGACAGGAT
158 T  V  S  W  N  S  G  A  L  T  S  G  V  H  T  F  P  A  V  L

601 CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG CAGCTTGGGC
    GTCAGGAGTC CTGAGATGAG GGAGTCGTCG CACCACTGGC ACGGGAGGTC GTCGAACCCG
178 Q  S  S  G  L  Y  S  L  S  S  V  V  T  V  P  S  S  S  L  G
```

FIG. 20A

```
661 ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA ACACCAAGGT GGACAAGAAA
    TGGGTCTGGA TGTAGACGTT GCACTTAGTG TTCGGGTCGT TGTGGTTCCA CCTGTTCTTT
198 T  Q  T  Y  I  C  N  V  N  H  K  P  S  N  T  K  V  D  K  K

721 GTTGAGCCCA AATCTTGTGA CAAAACTCAC ACATGA   (SEQ ID NO.26)
    CAACTCGGGT TTAGAACACT GTTTTGAGTG TGTACT
218 V  E  P  K  S  C  D  K  T  H  T  O        (SEQ ID NO.27)
```

FIG. 20B

Light Chain Primers:

MKLC-1, 22mer

5' CAGTCCAACTGTTCAGGACGCC 3' (SEQ ID NO.1)

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3' (SEQ ID NO.2)

MKLC-3, 23mer

5' GAAGTTGATGTCTTGTGAGTGGC 3' (SEQ ID NO.3)

Heavy Chain Primers:

IGG2AC-1, 24mer

5' GCATCCTAGAGTCACCGAGGAGCC 3' (SEQ ID NO.4)

IGG2AC-2, 22mer

5' CACTGGCTCAGGGAAATAACCC 3' (SEQ ID NO.5)

IGG2AC-3, 22mer

5' GGAGAGCTGGGAAGGTGTGCAC 3' (SEQ ID NO.6)

FIG. 21

Light chain forward primer

6G4.light.Nsi 36-MER

```
5' CCAATGCATACGCT GAC ATC GTG ATG ACC CAG ACC CC  3' (SEQ ID NO.28)
                  T   T           T       T        (SEQ ID NO.29)
                                  A       A        (SEQ ID NO.30)
```

Light chain reverse primer

6G4.light.Mun 35-MER

```
5' AGA TGT CAA TTG CTC ACT GGA TGG TGG GAA GAT GG 3' (SEQ ID NO.31)
```

FIG. 22

Heavy chain forward primer

6G4.heavy.Mlu 32-MER

5' CAAACGCGTACGCT GAG ATC CAG CTG CAG CAG 3' (SEQ ID NO.32)
T C (SEQ ID NO.33)

Heavy chain reverse primer

SL002B 39-MER

5' CGATGGGCCCGG ATAGACCGATGGGGCTGTTGTTTTGGC 3' (SEQ ID NO.11)
T (SEQ ID NO.15)
A (SEQ ID NO.14)
G (SEQ ID NO.13)

FIG. 23

```
 70 G ATATCGTGAT GACACAGACA CCACTCTCCC TGCCTGTCAG TCTTGGAGAT
    C TATAGCACTA CTGTGTCTGT GGTGAGAGGG ACGGACAGTC AGAACCTCTA
  1 D  I  V  M   T  Q  T   P  L  S  L   P  V  S   L  G  D

121 CAGGCCTCCA TCTCTTGCAG ATCTAGTCAG AGCCTTGTAC ACGGTATTGG AAACACCTAT
    GTCCGGAGGT AGAGAACGTC TAGATCAGTC TCGGAACATG TGCCATAACC TTTGTGGATA
 18 Q  A  S  I   S  C  R   S  S  Q   S  L  V  H   G  I  G   N  T  Y
                        *   *  *  *   *  *  *  *   *  *  *   *  *  *
                                         CDR #1

181 TTACATTGGT ACCTGCAGAA GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC
    AATGTAACCA TGGACGTCTT CGGTCCGGTC AGAGGTTTCG AGGACTAGAT GTTTCAAAGG
 38 L  H  W  Y   L  Q  K   P  G  Q   S  P  K  L   L  I  Y   K  V  S
    *  *                                                    *  *  *
                                                            CDR #2

241 AACCGATTTT CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTCACA
    TTGGCTAAAA GACCCCAGGG TCTGTCCAAG TCACCGTCAC CTAGTCCCTG TCTAAAGTGT
 58 N  R  F  S   G  V  P   D  R  F   S  G  S  G   S  G  T   D  F  T
    *  *  *  *

301 CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC TCAAAGTACA
    GAGTCCTAGT CGTCTCACCT CCGACTCCTA GACCCTGAAA TAAAGACGAG AGTTTCATGT
 78 L  R  I  S   R  V  E   A  E  D   L  G  L  Y   F  C  S   Q  S  T
                                                       *   *  *  *
                                                          CDR #3

361 CATGTTCCGC TCACGTTCGG TGCTGGGACC AAGCTGGAGC TGAAACGGGC TGATGCTGCA
    GTACAAGGCG AGTGCAAGCC ACGACCCTGG TTCGACCTCG ACTTTGCCCG ACTACGACGT
 98 H  V  P  L   T  F  G   A  G  T   K  L  E  L   K  R  A   D  A  A
    *  *  *  *   *
                                             MunI
421 CCAACTGTAT CCATCTTCCC ACCATCCAGT GAGCAATTGA  (SEQ ID NO.34)
    GGTTGACATA GGTAGAAGGG TGGTAGGTCA CTCGTTAACT
118 P  T  V  S   I  F  P   P  S  S   E  Q  L  K  (SEQ ID NO.35)
```

FIG. 24

```
 70 G AGATTCAGCT GCAGCAGTCT GGACCTGAGC TGATGAAGCC TGGGGCTTCA
    C TCTAAGTCGA CGTCGTCAGA CCTGGACTCG ACTACTTCGG ACCCCGAAGT
  1 E  I  Q  L   Q  Q  S   G  P  E  L   M  K  P   G  A  S

121 GTGAAGATAT CCTGCAAGGC TTCTGGTTAT TCATTCAGTA GCCACTACAT GCACTGGGTG
    CACTTCTATA GGACGTTCCG AAGACCAATA AGTAAGTCAT CGGTGATGTA CGTGACCCAC
 18 V  K  I  S   C  K  A   S  G  Y   S  F  S  S   H  Y  M   H  W  V
                                              *   *  *  *   *
                                           CDR #1

181 AAGCAGAGCC ATGGAAAGAG CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA
    TTCGTCTCGG TACCTTTCTC GGAACTCACC TAACCGATGT AACTAGGAAG GTTACCACTT
 38 K  Q  S  H   G  K  S   L  E  W   I  G  Y  I   D  P  S   N  G  E
                                           *  *   *  *  *   *  *  *
                                                    CDR #2

241 ACTACTTACA ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC
    TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAACT GACATCTGTG TAGAAGGTCG
 58 T  T  Y  N   Q  K  F   K  G  K   A  T  L  T   V  D  T   S  S  S
    *  *  *  *   *  *  *   *  *

301 ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGCA
    TGTCGGTTGC ACGTAGAGTC GTCGGACTGT AGACTACTGA GACGTCAGAT AAAGACACGT
 78 T  A  N  V   H  L  S   S  L  T   S  D  D  S   A  V  Y   F  C  A

361 AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG TCTGGGGCGC AGGGACCACG
    TCTCCCCTGA TATCTATGTT GCCGCTGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC
 98 R  G  D  Y   R  Y  N   G  D  W   F  F  D   V   W  G  A   G  T  T
       *  *  *   *  *  *   *  *  *   *  *  *   *
                      CDR #3

     BstEII                                           ApaI
421 GTCACCGTCT CCTCCGCCAA AACCGACAGC CCCATCGGTC TATCCGGGCC
    CAGTGGCAGA GGAGGCGGAT TTGGCTGTCG GGGTAGCCAG ATAGGCCCGG
118 V  T  V  S   S  A  K   T  D  S   P  I  G  L   S  G  P

471 CATC  (SEQ ID NO.36)
    GTAG
135  I    (SEQ ID NO.37)
```

FIG. 25

5' CTTGGTGGAGGCGGAGGAGACG 3' (SEQ ID NO.38)

Mutagenesis Primer for 6G425VL

DS/VF 38MER

5' GAAACGGGCTGTTGCTGCACCAACTGTATTCATCTTCC 3' (SEQ ID NO.39)

SYN.BstEII 31 MER

5' GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 3' (SEQ ID NO.40)

SYN.Apa 22 MER

5' CTTGGTGGAGGCGGAGGAGACG 3' (SEQ ID NO.38)

FIG. 26

```
  1 ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAT
    TACTTCTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA
-23 M  K  K  N   I  A  F   L  L  A   S  M  F  V   F  S  I   A  T  N

 61 GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCCC TGCCTGTCAG TCTTGGAGAT
    CGTATGCGAC TATAGCACTA CTGTGTCTGT GGTGAGAGGG ACGGACAGTC AGAACCTCTA
 -3 A  Y  A  D   I  V  M   T  Q  T   P  L  S  L   P  V  S   L  G  D

121 CAGGCCTCCA TCTCTTGCAG ATCTAGTCAG AGCCTTGTAC ACGGTATTGG AAACACCTAT
    GTCCGGAGGT AGAGAACGTC TAGATCAGTC TCGGAACATG TGCCATAACC TTTGTGGATA
 18 Q  A  S  I   S  C  R   S  S  Q   S  L  V  H   G  I  G   N  T  Y
                     *      *  *  *   *  *  *  *   *  *  *   *  *  *
                                        CDR #1

181 TTACATTGGT ACCTGCAGAA GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC
    AATGTAACCA TGGACGTCTT CGGTCCGGTC AGAGGTTTCG AGGACTAGAT GTTTCAAAGG
 38 L  H  W  Y   L  Q  K   P  G  Q   S  P  K  L   L  I  Y   K  V  S
    *  *                                                      *  *  *
                                                             CDR #2

241 AACCGATTTT CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTCACA
    TTGGCTAAAA GACCCCAGGG TCTGTCCAAG TCACCGTCAC CTAGTCCCTG TCTAAAGTGT
 58 N  R  F  S   G  V  P   D  R  F   S  G  S  G   S  G  T   D  F  T
    *  *  *  *
301 CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC TCAAAGTACA
    GAGTCCTAGT CGTCTCACCT CCGACTCCTA GACCCTGAAA TAAAGACGAG AGTTTCATGT
 78 L  R  I  S   R  V  E   A  E  D   L  G  L  Y   F  C  S   Q  S  T
                                                    *  *  *  *
                                                    CDR #3

361 CATGTTCCGC TCACGTTCGG TGCTGGGACC AAGCTGGAGC TGAAACGGGC TGTTGCTGCA
    GTACAAGGCG AGTGCAAGCC ACGACCCTGG TTCGACCTCG ACTTTGCCCG ACAACGACGT
 98 H  V  P  L   T  F  G   A  G  T   K  L  E  L   K  R  A   V  A  A
    *  *  *  *   *
421 CCAACTGTAT TCATCTTCCC ACCATCCAGT GAGCAATTGA AATCTGGAAC TGCCTCTGTT
    GGTTGACATA AGTAGAAGGG TGGTAGGTCA CTCGTTAACT TTAGACCTTG ACGGAGACAA
118 P  T  V  F   I  F  P   P  S  S   E  Q  L  K   S  G  T   A  S  V

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
    CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
138 V  C  L  L   N  N  F   Y  P  R   E  A  K  V   Q  W  K   V  D  N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
    CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCGTGG
158 A  L  Q  S   G  N  S   Q  E  S   V  T  E  Q   D  S  K   D  S  T

601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
    ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y  S  L  S   S  T  L   T  L  S   K  A  D  Y   E  K  H   K  V  Y
```

FIG. 27A

```
661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
    CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT
198 A  C  E  V  T  H  Q  G  L  S  S  P  V  T  K  S  F  N  R  G

721 GAGTGTTAA  (SEQ ID NO.41)
    CTCACAATT
218 E  C  O    (SEQ ID NO.42)
```

FIG. 27B

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M  K  K  N   I  A  F   L  L  A   S  M  F  V   F  S  I   A  T  N

 61 GCGTACGCTG AGATTCAGCT GCAGCAGTCT GGACCTGAGC TGATGAAGCC TGGGGCTTCA
    CGCATGCGAC TCTAAGTCGA CGTCGTCAGA CCTGGACTCG ACTACTTCGG ACCCCGAAGT
 -3 A  Y  A  E   I  Q  L   Q  Q  S   G  P  E  L   M  K  P   G  A  S

121 GTGAAGATAT CCTGCAAGGC TTCTGGTTAT TCATTCAGTA GCCACTACAT GCACTGGGTG
    CACTTCTATA GGACGTTCCG AAGACCAATA AGTAAGTCAT CGGTGATGTA CGTGACCCAC
 18 V  K  I  S   C  K  A   S  G  Y   S  F  S  S   H  Y  M   H  W  V
                                      *  *  *  *   *
                                      CDR #1

181 AAGCAGAGCC ATGGAAAGAG CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA
    TTCGTCTCGG TACCTTTCTC GGAACTCACC TAACCGATGT AACTAGGAAG GTTACCACTT
 38 K  Q  S  H   G  K  S   L  E  W   I  G  Y  I   D  P  S  N  G  E
                                      *  *  *  *  *  *  *  *  *
                                                CDR #2

241 ACTACTTACA ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC
    TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAACT GACATCTGTG TAGAAGGTCG
 58 T  T  Y  N   Q  K  F   K  G  K   A  T  L  T   V  D  T   S  S  S
    *  *  *  *   *  *  *   *  *
301 ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGCA
    TGTCGGTTGC ACGTAGAGTC GTCGGACTGT AGACTACTGA GACGTCAGAT AAAGACACGT
 78 T  A  N  V   H  L  S   S  L  T   S  D  D  S   A  V  Y   F  C  A

361 AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG TCTGGGGCGC AGGGACCACG
    TCTCCCCTGA TATCTATGTT GCCGCTGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC
 98 R  G  D  Y   R  Y  N   G  D  W   F  F  D  V   W  G  A   G  T  T
       *  *  *   *  *  *   *  *  *   *  *  *  *
                  CDR #3

421 GTCACCGTCT CCTCCGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC
    CAGTGGCAGA GGAGGCGGAG GTGGTTCCCG GGTAGCCAGA AGGGGGACCG TGGGAGGAGG
118 V  T  V  S   S  A  S   T  K  G   P  S  V  F   P  L  A   P  S  S

481 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA
    TTCTCGTGGA GACCCCCGTG TCGCCGGGAC CCGACGGACC AGTTCCTGAT GAAGGGGCTT
138 K  S  T  S   G  G  T   A  A  L   G  C  L  V   K  D  Y   F  P  E

541 CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGCACAC CTTCCCGGCT
    GGCCACTGCC ACAGCACCTT GAGTCCGCGG GACTGGTCGC CGCACGTGTG GAAGGGCCGA
158 P  V  T  V   S  W  N   S  G  A   L  T  S  G   V  H  T   F  P  A

601 GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC
    CAGGATGTCA GGAGTCCTGA GATGAGGGAG TCGTCGCACC ACTGGCACGG GAGGTCGTCG
178 V  L  Q  S   S  G  L   Y  S  L   S  S  V  V   T  V  P   S  S  S
```

FIG. 28A

```
661 TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC
    AACCCGTGGG TCTGGATGTA GACGTTGCAC TTAGTGTTCG GGTCGTTGTG GTTCCACCTG
198 L  G  T  Q   T  Y  I   C  N  V   N  H  K  P   S  N  T   K  V  D

721 AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GA  (SEQ ID NO.43)
    TTCTTTCAAC TCGGGTTTAG AACACTGTTT TGAGTGTGTA CT
218 K  K  V  E   P  K  S   C  D  K   T  H  T  O     (SEQ ID NO.44)
```

FIG. 28B

Variable Light Chain Domain

```
                 10        20       abcde 30        40
6G425     DIVMTQTPLSLPVSLGDQASISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIY
           #   # #  ## #  ### #                    #    ##
F(ab)-1   DIQMTQSPSSLSASVGDRVTITCRSSQSLVHGIGNTYLHWYQQKPGKAPKLLIY
                              # ##########
humκI     DIQMTQSPSSLSASVGDRVTITCRASKTI-----SKYLAWYQQKPGKAPKLLIY
                              ============
                             +++++++++++++++
                                    L1

          50        60        70        80        90        100
6G425     YKVSNRFSGVPDRFSDSGSGTDFTLRISRVEAEDLGLYFCSQSTHVPLTFGAGTKLELKR (SEQ ID NO.45)
                   #   #          #  ##### ### #            #   # #
F(ab)-1   YKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQSTHVPLTFGQGTKVEIKR (SEQ ID NO.46)
           ## ###                                  # ####
humκI     YSGSTLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR (SEQ ID NO.47)
           ===                                      ======
           +++++++                                +++++++++
              L2                                      L3
```

Variable Heavy Chain Domain

```
                 10        20        30        40
6G425     EIQLQQSGPELMKPGASVKISCKASGYSFSSHYMHWVKQSHGKSLEWI
           #  ##  ## ##  # ###  #               # ##  #   #
F(ab)-1   EVQLVESGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWV
                             #  ## # #
humIII    EVQLVESGGGLVQPGGSLRLSCAASGFSFTGHWMNWVRQAPGKGLEWV
                             =======
                                  +++++
                                  H1

          50  a                 70        80  abc       90        100       110
6G425     GYIDPSNGETTYNQKFKGKATLTVDTSSSTANVHLSSLTSDDSAVYFCAARGDYRYNGDWFFDVWGAGT (SEQ ID NO.48)
                        ## ### # ## ######  ### #   #                    #
F(ab)-1   GYIDPSNGETTYNQKFKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAARGDYRYNGDWFFDVWGQGT (SEQ ID NO.49)
           # #  ##  # ####                                # # # ###  #
humIII    GMIHPSDSETRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAARGIYFY-GTTYFDYWGQGT (SEQ ID NO.50)
              ====                                        ===========
           ++++++++++++++++                              ++++++++++++
                 H2                                          H3
```

FIG. 29

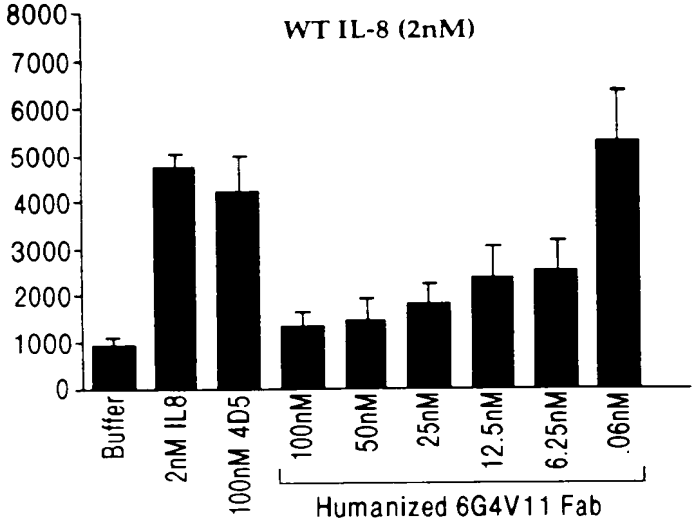


FIG. 30A

IC50~12nM

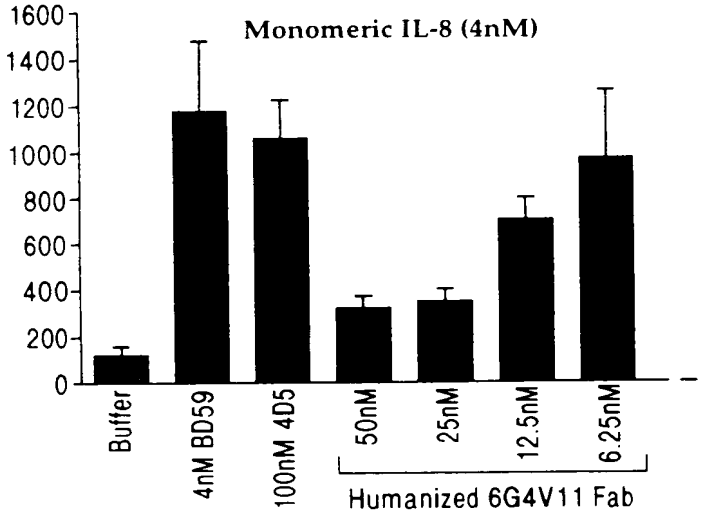


FIG. 30B

IC50~15nM

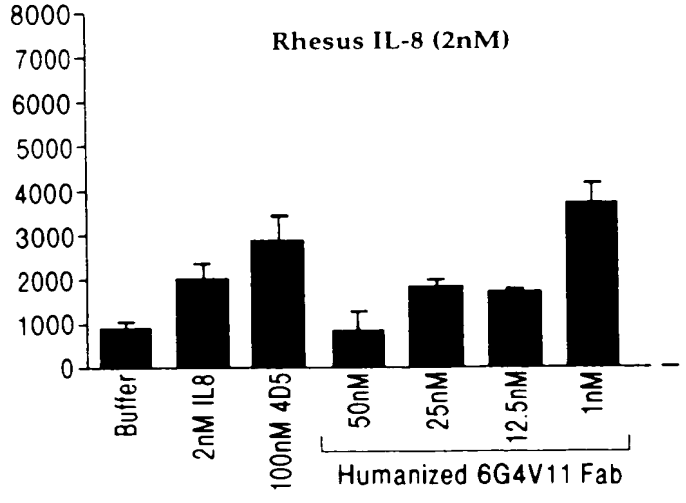


FIG. 30C

IC50~22nM

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Light Chain

MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRVTITCRSSQSLVHGIGNTY
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQST
HVPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC (SEQ ID NO.51)

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Heavy Chain

MKKNIAFLLASMFVFSIATNAYAEVQLV**Q**SGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVRQAPGKGLEWVGYIDPSNGETTYNQKFKGRFT**L**SRDNSKNT**A**YLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHT (SEQ ID NO.52)

Amino Acid Sequence of the peptide linker and M13 Phage Coat (gene-III)

SGGGSGSGDFDYEKMANANKGAMTENADENALQSDAKGKLDSVATDYGAAIDGFIGDVS
GLANGNGATGDFAGSSNSQMAQVGDGDNSPLMNNFRQYLPSLPQSVECRPFVFSAGKPY
EFSIDCDKINLFRGVFAFLLYVATFMYVFSTFANILRNKES (SEQ ID NO.53)

FIG. 31A

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M  K  K  N   I  A  F   L  L  A   S  M  F  V   F  S  I   A  T  N

 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
    CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
 -3 A  Y  A  D   I  Q  M   T  Q  S   P  S  S  L   S  A  S   V  G  D

121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TAACACGTAT
    TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACGATGCATA
 18 R  V  T  I   T  C  R   S  S  Q   S  L  V  H   G  I  G   N  T  Y

181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
    AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
 38 L  H  W  Y   Q  Q  K   P  G  K   A  P  K  L   L  I  Y   K  V  S

241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
    TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
 58 N  R  F  S   G  V  P   S  R  F   S  G  S  G   S  G  T   D  F  T

301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT
    GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
 78 L  T  I  S   S  L  Q   P  E  D   F  A  T  Y   Y  C  S   Q  S  T

361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
    GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
 98 H  V  P  L   T  F  G   Q  G  T   K  V  E  I   K  R  T   V  A  A

421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
    GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
118 P  S  V  F   I  F  P   P  S  D   E  Q  L  K   S  G  T   A  S  V

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
    CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
138 V  C  L  L   N  N  F   Y  P  R   E  A  K  V   Q  W  K   V  D  N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
    CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCGTGG
158 A  L  Q  S   G  N  S   Q  E  S   V  T  E  Q   D  S  K   D  S  T

601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
    ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y  S  L  S   S  T  L   T  L  S   K  A  D  Y   E  K  H   K  V  Y

661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
    CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT
198 A  C  E  V   T  H  Q   G  L  S   S  P  V  T   K  S  F   N  R  G
                                                                (SEQ ID NO:54)
721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
    CTCACAATTC GACTAGGAGA TGCGGCCTGC GTAGCACCGG GATCATGCGT TGATCAGCAT
218 E  C  O (SEQ ID NO:51)
```

FIG. 31B

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Light Chain

MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRVTITCRSSQSLVHGIGNTY
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQST
HVPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC (SEQ ID NO.51)

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Heavy Chain

MKKNIAFLLASMFVFSIATNAYAEVQLVESGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVKQ**A**PGKGLEWVGYIDPSNGETTYNQKFKGRFT**L**SRDNSKNT**A**YLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHT (SEQ ID NO.55)

FIG. 31C

FIG. 32

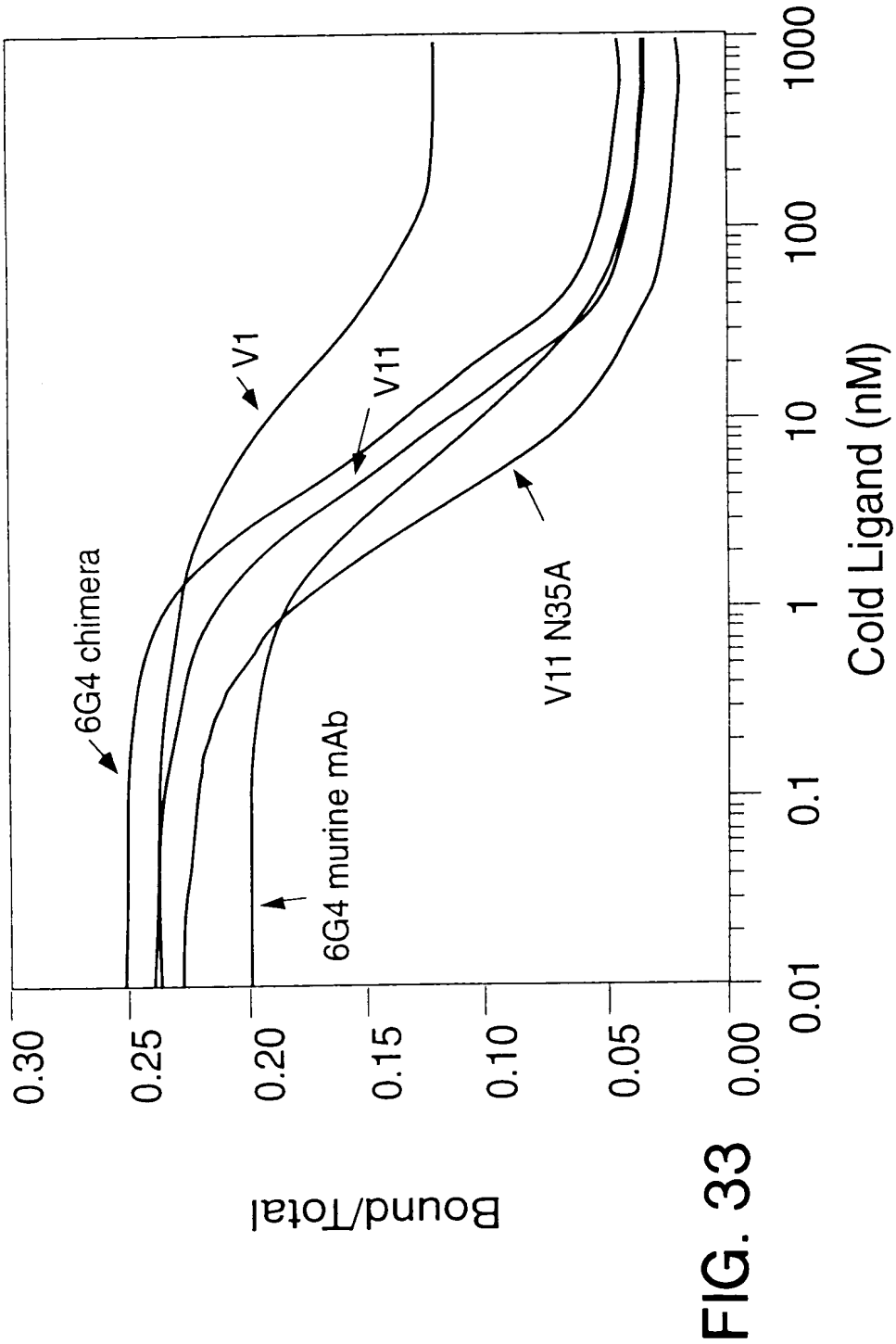


FIG. 33

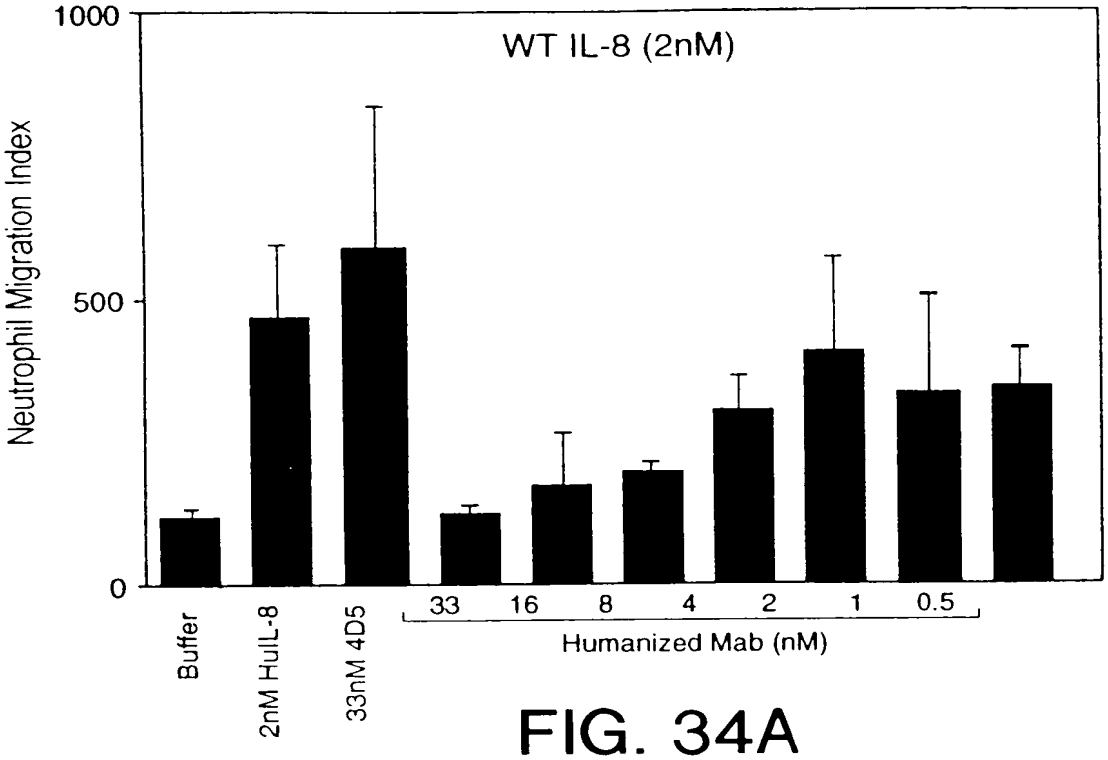


FIG. 34A

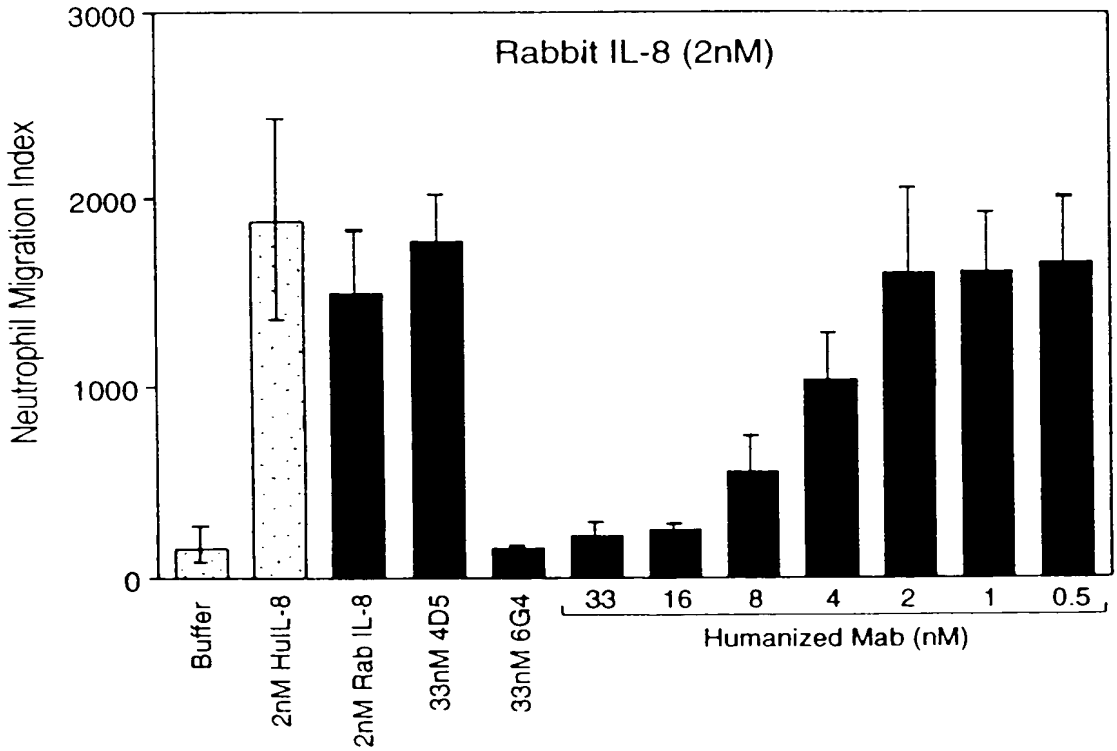


FIG. 34B

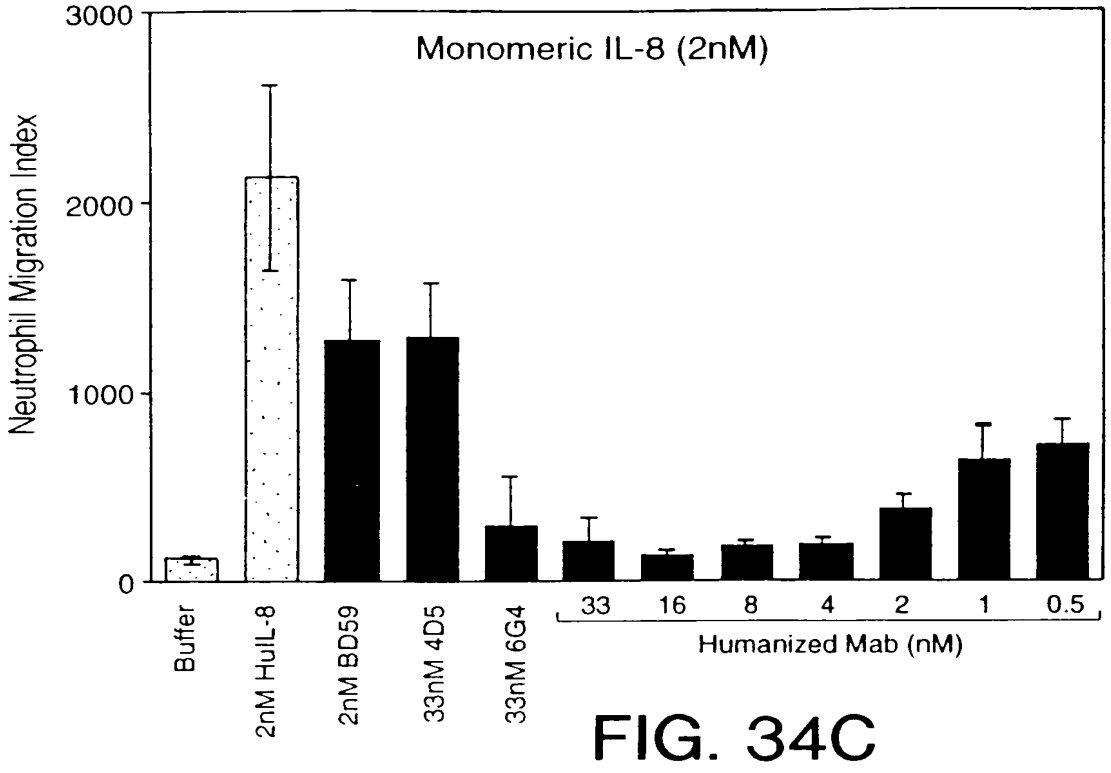


FIG. 34C

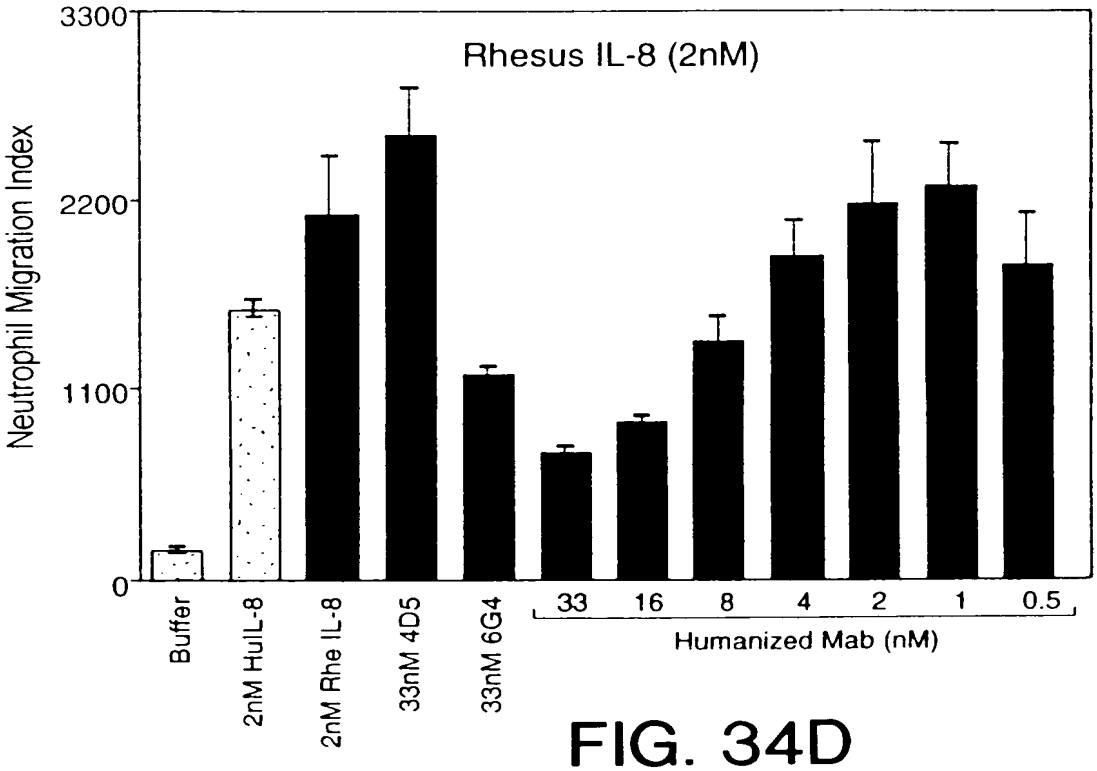


FIG. 34D

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Light Chain

MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRVTITCRSSQSLVHGIG**A**TY
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQST
HVPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC (SEQ ID NO.56)

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Heavy Chain

MKKNIAFLLASMFVFSIATNAYAEVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVRQAPGKGLEWVGYIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHT (SEQ ID NO.52)

Amino Acid Sequence of the putative Pepsin Cleavage Site and GCN4 Leucine Zipper

CPPCPAPE<u>LL</u>GGRMKQLEDKVEELLSKNYHLENEVARLKKLVGER (SEQ ID NO.57)

FIG. 35

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M  K  K  N   I  A  F   L  L  A   S  M  F  V   F  S  I   A  T  N

 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
    CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
 -3 A  Y  A  D   I  Q  M   T  Q  S   P  S  S  L   S  A  S   V  G  D

121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGCTACGTAT
    TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACGATGCATA
 18 R  V  T  I   T  C  R  S  S  Q   S  L  V  H   G  I  G   A  T  Y

181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
    AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
 38 L  H  W  Y   Q  Q  K   P  G  K   A  P  K  L   L  I  Y   K  V  S

241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
    TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
 58 N  R  F  S   G  V  P   S  R  F   S  G  S  G   S  G  T   D  F  T

301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT
    GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
 78 L  T  I  S   S  L  Q   P  E  D   F  A  T  Y   Y  C  S   Q  S  T

361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
    GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
 98 H  V  P  L   T  F  G   Q  G  T   K  V  E  I   K  R  T   V  A  A

421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
    GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
118 P  S  V  F   I  F  P   P  S  D   E  Q  L  K   S  G  T   A  S  V

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
    CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
138 V  C  L  L   N  N  F   Y  P  R   E  A  K  V   Q  W  K   V  D  N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
    CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCGTGG
158 A  L  Q  S   G  N  S   Q  E  S   V  T  E  Q   D  S  K   D  S  T

601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
    ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y  S  L  S   S  T  L   T  L  S   K  A  D  Y   E  K  H   K  V  Y

661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
    CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT
198 A  C  E  V   T  H  Q   G  L  S   S  P  V  T   K  S  F   N  R  G
                                                              (SEQ ID NO.58)
721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
    CTCACAATTC GACTAGGAGA TGCGGCCTGC GTAGCACCGG GATCATGCGT TGATCAGCAT
218 E  C  O (SEQ ID NO.56)
```

FIG. 36

```
781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCTTGCA
    TTTTCCCATA GATCTCCAAC TCCACTAAAA TACTTTTTCT TATAGCGTAA AGAAGAACGT
 -1                                   M  K  K  N   I  A  F   L  L  A

841 TCTATGTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG AGGTTCAGCT AGTGCAGTCT
    AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA
-11 S  M  F  V   F  S  I   A  T  N   A  Y  A  E   V  Q  L   V  Q  S

901 GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC
    CCGCCACCGG ACCACGTCGG TCCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG
 8  G  G  G  L   V  Q  P   G  G  S   L  R  L  S   C  A  A   S  G  Y

961 TCCTTCTCGA GTCACTATAT GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG
    AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTCCC GGACCTTACC
 28 S  F  S  S   H  Y  M   H  W  V   R  Q  A  P   G  K  G   L  E  W

1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT
     CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAA GTTCCCGGCA
 48  V  G  Y  I   D  P  S   N  G  E   T  T  Y  N   Q  K  F   K  G  R

1081 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT
     AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA
 68  F  T  L  S   R  D  N   S  K  N   T  A  Y  L   Q  M  N   S  L  R

1141 GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT ATCGCTACAA TGGTGACTGG
     CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCCTAA TAGCGATGTT ACCACTGACC
 88  A  E  D  T   A  V  Y   Y  C  A   R  G  D  Y   R  Y  N   G  D  W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCTC CACCAAGGGC
     AAGAAGCTGC AGACCCCAGT TCCTTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCG
 108 F  F  D  V   W  G  Q   G  T  L   V  T  V  S   S  A  S   T  K  G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG
     GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCCGTG TCGCCGGGAC
 128 P  S  V  F   P  L  A   P  S  S   K  S  T  S   G  G  T   A  A  L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC
     CCGACGGACC AGTTCCTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG
 148 G  C  L  V   K  D  Y   F  P  E   P  V  T  V   S  W  N   S  G  A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC
     GACTGGTCGC CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCCTGA GATGAGGGAG
 168 L  T  S  G   V  H  T   F  P  A   V  L  Q  S   S  G  L   Y  S  L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG
     TCGTCGCACC ACTGGCACGG GAGGTCGTCG AACCCGTGGG TCTGGATGTA GACGTTGCAC
 188 S  S  V  V   T  V  P   S  S  S   L  G  T  Q   T  Y  I   C  N  V

1501 AATCACAAGC CCAGCAACAC CAAGGTCGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA
     TTAGTGTTCG GGTCGTTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT
 208 N  H  K  P   S  N  T   K  V  D   K  K  V  E   P  K  S   C  D  K

1561 ACTCACACAT GCCCGCCGTG CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA
     TGAGTGTGTA CGGGCGGCAC GGGTCGTGGT CTTGACGACC CGCCGGCGTA CTTTGTCGAT
 228 T  H  T  C   P  P  C   P  A  P   E  L  L  G   G  R  M   K  Q  L
```

FIG. 37A

```
1621 GAGGACAAGG TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA
     CTCCTGTTCC AGCTTCTCGA TGAGAGGTTC TTGATGGTGG ATCTCTTACT TCACCGTTCT
 248 E  D  K  V   E  E  L   L  S  K   N  Y  H  L   E  N  E   V  A  R

1681 CTCAAAAAGC TTGTCGGGGA GCGCTAA   (SEQ ID NO.59)
     GAGTTTTTCG AACAGCCCCT CGCGATT
 268 L  K  K  L   V  G  E   R  O     (SEQ ID NO.60)
```

FIG. 37B

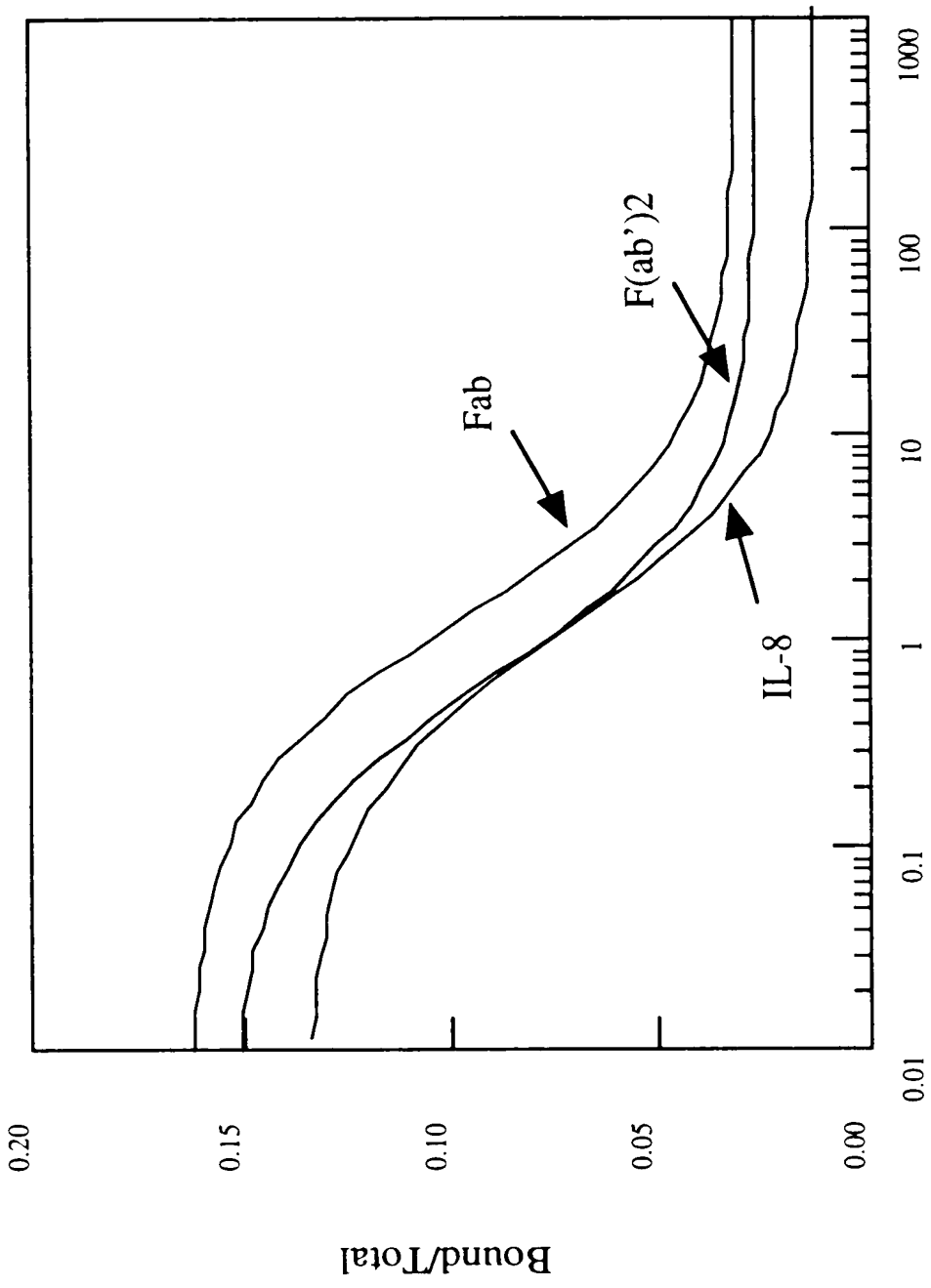


FIG. 38

FIG. 39

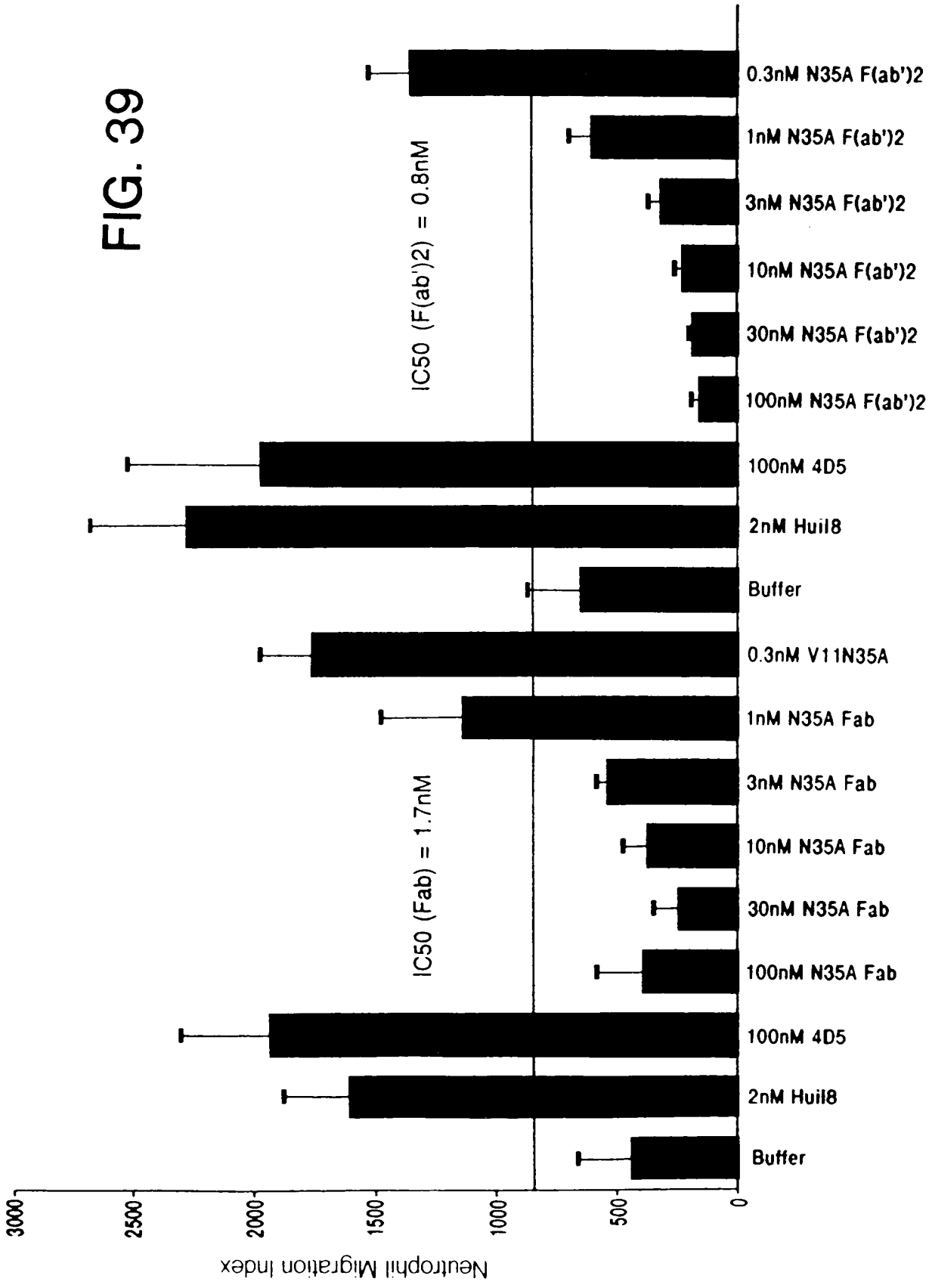
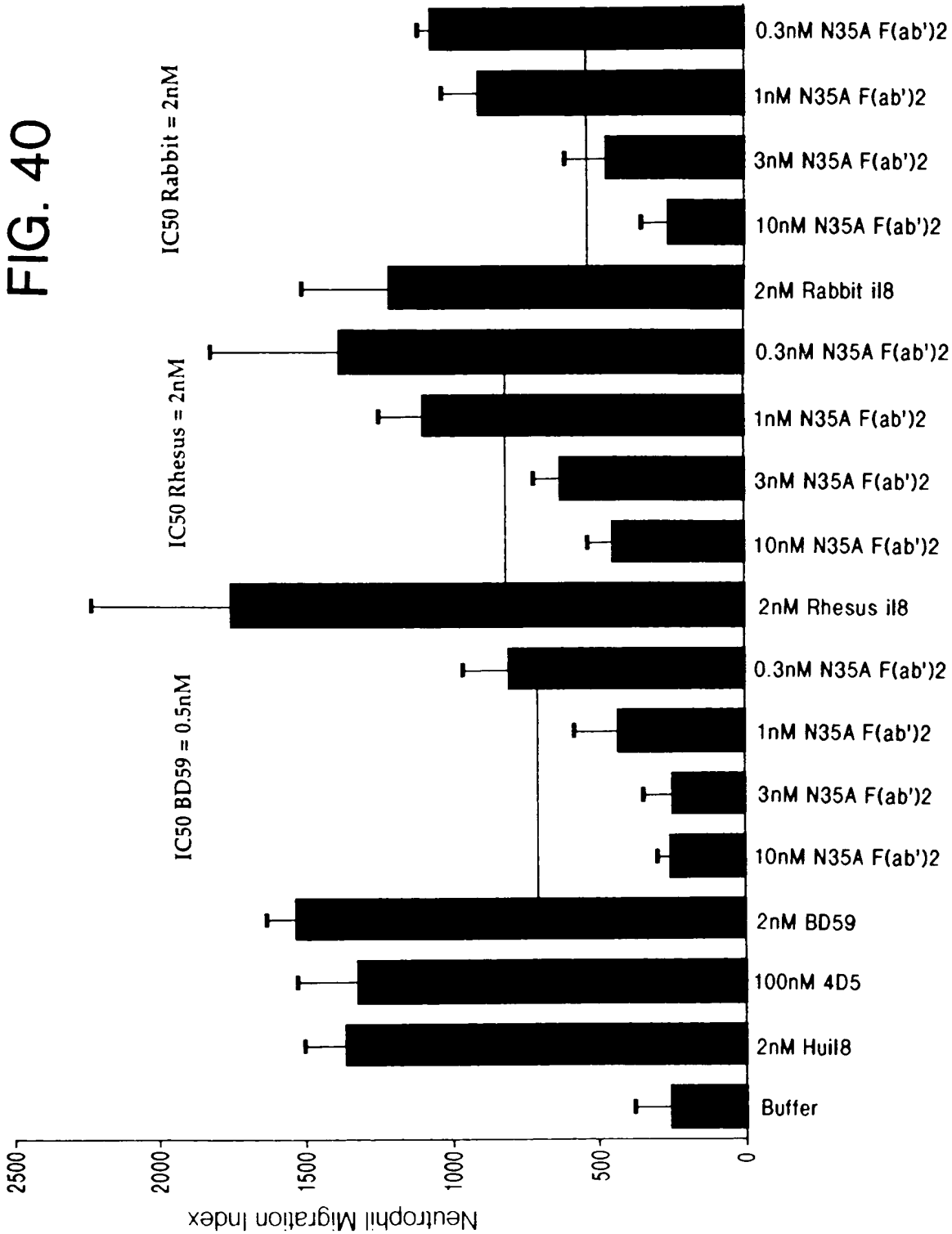


FIG. 40



```
                                                                                  aluI                  pleI
                                                                                 hindIII            mboII   taqI
    ecoRI         pflMI                                          ddeI         tru9I                 earI/ksp632I
    apoI          bslI                        nlaIII        bsrDI             mseI cac8I         mboII  hinfI
  1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
    CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

                bspMI                                                                              sau3AI
             hinPI                                                                                 mboI/ndeII[dam-]
             hhaI/cfoI                                                                             dpnI[dam+]
            mstI          aluI               mslI                     hinPI             aciI       dpnII[dam-]
            aviII/fspI  hindIII            maeIII bsrDI               hhaI/cfoI       nspBII      bclI[dam-]  mnlI
101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
    CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

                                                                    thaI
                                                                    fnuDII/mvnI
                                                                fnu4HI
                                                                bsoFI
                                                                bbvI        maeII
           rsaI                                              fnu4HI bstUI  snaBI
      hinPI                                                  bsoFI  bsh1236I                         mnlI
      hhaI/cfoI  mnlI           cac8I                        bbvI  hinPI   bsaAI                  fokI
     haeII csp6I             sfaNI   bsmI                   aluI   hhaI/cfoI                     sfaNI
201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
    CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

                                                                                                              aluI
                                                                                                              sstI
                                                                                                              sacI
                                                                                                              hgiJII
                                              haeIII/palI                                                     hgiAI/aspHI
                                             mcrI                                                             ecl136II
                                             eagI/xmaIII/eclXI                                         ecoRI  bsp1286
                                             eaeI                                              rmaI       bsiHKAI
                        aluI                 cfrI                                              maeI       bmyI
         tru9I         pvuII                 bsiEI   ahdI/eam1105I                tru9I        bfaI    taqI
         mseI          nspBII            maeIII    bsmAI                          mseI        maeIII  apoI   banII
301 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GAATTCGAGC
    TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CTTAAGCTCG
```

FIG. 41A

```
          scrFI
          nciI
          mspI
          hpaII
          dsaV
         xmaI/pspAI
         smaI
         scrFI
         nciI
         dsaV
         cauII        xhoI
         bsaJI     mnlI
         avaI   sau3AI taqI
       rsaI      mboI/ndeII[dam-]
       csp6I     dpnI[dam+]
      nlaIV     nlaIV  paeR7I
      kpnI cauII dpnII[dam-]
      hgiCI     bstYI/xhoII
      banI bsaJI alwI[dam-]
      asp718    bamHI  avaI        hphI
      acc65I    alwI[dam-] mnlI  mnlI                                  mboII   sfaNI
401 TCGGTACCCG GGGATCCTCT CGAGGTTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTC TTCTTGCATC TATGTTCGTT TTTTCTATTG CTACAAACGC
    AGCCATGGGC CCCTAGGAGA GCTCCAACTC CACTAAAATA CTTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA AAAAGATAAC GATGTTTGCG
-23                                        M   K   K   N   I   A   F   L   L   A   S   M   F   V   F   S   I   A   T   N   A
      a mutation was found that inactivated the mluI site.  The penultimate nucleotide was changed fr G toT ^

                                    sstI
                                    sacI
                                    hgiJII
                                    hgiAI/aspHI
                                    ecl136II                                                  bspMI
                                    bsp1286                                                 scfI
                                    bsiHKAI                                                 pstI
                               bsmFI  bmyI                                        hphI      sse8387I             ddeI   nlaIII
                            bsrI  avaI aluI          mnlI                      maeIII    bspMI              aluI   rsaI
          ecoRV       tth111I/aspI  banII       aciI                        bstEII  hphI bsgI            hindIII csp6I
501 ATACGCTGAT ATCCAGATGA CCCAGTCCCC GAGCTCCCTG TCCGCCTCTG TGGGCGATAG GGTCACCATC ACCTGCAGGT CAAGTCAAAG CTTAGTACAT
    TATGCGACTA TAGGTCTACT GGGTCAGGGG CTCGAGGGAC AGGCGGAGAC ACCCGCTATC CCAGTGGTAG TGGACGTCCA GTTCAGTTTC GAATCATGTA
 -2  Y   A   D   I   Q   M   T   Q   S   P   S   S   L   S   A   S   V   G   D   R   V   T   I   T   C   R   S   S   Q   S   L   V   H
```

FIG. 41B

```
                                          scrFI
                                          mvaI                                                    tfiI
                                          ecoRII                                        hinfI       bsmFI
                                          dsaV                                        taqI    bpmI/gsuI[dcm-]
                                          bstNI    aluI                                  claI/bsp106   pleI
                          bsrI            apyI[dcm+]                                     bspDI[dam-]   hinfI
601 GGTATAGGTG CTACGTATTT ACACTGGTAT CAACAGAAAC CAGGAAAAGC TCCGAAACTA CTGATTTACA AAGTATCCAA TCGATTCTCT GGAGTCCCTT
    CCATATCCAC GATGCATAAA TGTGACCATA GTTGTCTTTG GTCCTTTTCG AGGCTTTGAT GACTAAATGT TTCATAGGTT AGCTAAGAGA CCTCAGGGAA
 32 G  I  G  A  T  Y  L  H  W  Y  Q  Q  K  P  G  K  A  P  K  L  L  I  Y  K  V  S  N  R  F  S  G  V  P  S

                   mspI
                   hpaII
                   bslI
                  bsaWI
                 sau3AI
                 mboI/ndeII[dam-]
                 dpnI[dam+]
                 dpnII[dam-]                                    fnu4HI
                 alwI[dam-]                                     bsoFI
                nlaIV                                           bbvI
                bstYI/xhoII                                   scfI      mboII                                  rsaI
                bamHI                                         pstI      bpuAI                                  csp6I
                alwI[dam-]   bsmFI                            bsgI      bbsI                                 scaI  nlaIII
701 CTCGCTTCTC TGGATCCGGT TCTGGGACGG ATTTCACTCT GACCATCAGC AGTCTGCAGC CAGAAGACTT CGCAACTTAT TACTGTTCAC AGAGTACTCA
    GAGCGAAGAG ACCTAGGCCA AGACCCTGCC TAAAGTGAGA CTGGTAGTCG TCAGACGTCG GTCTTCTGAA GCGTTGAATA ATGACAAGTG TCTCATGAGT
 66   R  F  S   G  S  G   S  G  T  D   F  T  L   T  I  S   S  L  Q  P   E  D  F   A  T  Y   Y  C  S  Q   S  T  H

                            styI
                            bsaJI
                          rsaI
                          csp6I
                         nlaIV
                         kpnI
                         hgiCI          sau3AI
       bsrBI              banI           mboI/ndeII[dam-]  fnu4HI        mboII
       aciI               asp718         dpnI[dam+]        bsoFI       bpuAI       aciI
    bsmFI     maeII       acc65I         dpnII[dam-]       bbvI        bbsI    mboII
801 TGTCCCGCTC ACGTTTGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA
    ACAGGGCGAG TGCAAACCTG TCCCATGGTT CCACCTCTAG TTTGCTTGAC ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT
 99  V  P  L   T  F  G  Q   G  T  K   V  E  I   K  R  T  V   A  A  P   S  V  F   I  F  P  P   S  D  E   Q  L  K
```

FIG. 41C

```
                                                                                                                   scrFI
                                                                                                                   mvaI
                                                                                                                   ecoRII
                                                                                                                   dsaV
                                                                  haeIII/palI                                      bstNI
         xmnI                       xmnI                         haeI       rsaI                      mnlI        bsaJI
         asp700            cac8I    asp700                      mnlI        csp6I                     bslI    maeIII apyI[dcm+]
901  TCTGGAACTG CTTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC
     AGACCTTGAC GAAGACAACA CACGGACGAC TTATTGAAGA TAGGGTCTCT CCGGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTTAGC CCATTGAGGG
132  S  G  T  A   S  V  V   C  L  L   N  N  F  Y   P  R  E   A  K  V   Q  W  K  V   D  N  A   L  Q  S   G  N  S  Q

                                                                fnu4HI
                                                                bsoFI          celII/espI
                                                            ddeI               blpI/bpu1102I
            maeIII                                   scfI   mnlI bbvI      hgaI ddeI                             accI  cac8I
1001 AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC
     TCCTCTCACA GTGTCTCGTC CTGTCGTTCC TGTCGTGGAT GTCGGAGTCG TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTGT TTCAGATGCG
166   E  S  V   T  E  Q   D  S  K  D   S  T  Y   S  L  S   S  T  L  T   L  S  K   A  D  Y   E  K  H  K   V  Y  A

                           cac8I
                          aluI
                          sstI
                          sacI
                          hgiJII
                          hgiAI/aspHI
                          ecl136II
                          bsp1286
                          bsiHKAI
                          bmyI                                                         mnlI                       rmaI
                    haeIII/palI                                                     sau3AI                        maeI
                   sau96I banII                                                     mboI/ndeII[dam-]              bfaI
                   asuI ddeI                                                  aluI  dpnI[dam+]       hgaI       sau96I
          hphI    eco0109I/draII                                          tru9I     dpnII[dam-] mspI          haeIII/palI
         maeIII   alwNI[dcm-]           maeIII     aluI                   mseI      alwI[dam-]  hpaII sfaNI   asuI
1101 CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA ACAGGGGAGA GTGTTAAGCT GATCCTCTAC GCCGGACGCA TCGTGGCCCT
     GACGCTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT TGTCCCCTCT CACAATTCGA CTAGGAGATG CGGCCTGCGT AGCACCGGGA
199   C  E  V   T  H  Q  G   L  S  S   P  V  T   K  S  F  N   R  G  E   C  O (SEQ ID NO.56)
```

FIG. 41D

```
            rmaI                rmaI
            maeI                maeI
     rsaI   bfaI                bfaI        hphI
     csp6I  speI                xbaI mnlI  mnlI                                mboII   sfaNI
1201 AGTACGCAAC TAGTCGTAAA AAGGGTATCT AGAGGTTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTC TTCTTGCATC TATGTTCGTT TTTTCTATTG
     TCATGCGTTG ATCAGCATTT TTCCCATAGA TCTCCAACTC CACTAAAATA CTTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA AAAAGATAAC
 -23                                                    M   K   K   N   I   A   F   L   L   A   S   M   F   V   F   S   I   A

                                                                scrFI
                                                                mvaI
                                                                ecoRII
                                                                dsaV

              rsaI                                  scrFI
             bsiWI/splI                             mvaI   fnu4HI
           thaI                                     ecoRII
           fnuDII/mvnI                              dsaV bstNI hgiJII                    aluI
           bstUI                rmaI                bstNI  bsoFI     bspl286                alwNI[dcm-]
           bsh1236I             maeI                apyI[dcm+] bsaJI bmyI                  fnu4HI
          mluI csp6I  mnlI      bfaI              haeIII/palI  apyI[dcm+]                  bsoFI
          aflIII    ddeI      aluI           aciI haeI      bbvI      banII                 bbvI
1301 CTACAAACGC GTACGCTGAG GTTCAGCTAG TGCAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT CTGGCTACTC
     GATGTTTGCG CATGCGACTC CAAGTCGATC ACGTCAGACC GCCACCGGAC CACGTCGGTC CCCCGAGTGA GGCAAACAGG ACACGTCGAA GACCGATGAG
  -5   T   N   A   Y   A   E   V   Q   L   V   Q   S   G   G   G   L   V   Q   P   G   G   S   L   R   L   S   C   A   A   S   G   Y   S

                                    scrFI
                                    nciI
                                    mspI
                                    hpaII
                                    dsaV
                                    cauII
                                    bslI
                                   xmaI/pspAI
                                   smaI
                                   scrFI
                                   nciI
                                   dsaV          scrFI
                                   cauII         mvaI
                                   bslI          ecoRII
```

FIG. 41E

```
                                    bsaJI        dsaV
                                     avaI        bstNI
                                    bsaJI        bslI                    bslI
         pleI                sau96I sau96I       apyI[dcm+]             sau3AI
         hinfI               avaII  nlaIV       sau96I             mboI/ndeII[dam-]
        taqI                 asuI   haeIII/palI asuI                    dpnI[dam+]               maeII
       xhoI                 nlaIV   asuI       eco0109I/draII      dpnII[dam-]        snaBI
       paeR7I              bsrI    eco0109I/draII haeIII/palI          alwI[dam-]   hphI      bsaAI
       avaI maeIII
1401 CTTCTCGAGT CACTATATGC ACTGGGTCCG TCAGGCCCCG GGTAAGGGCC TGGAATGGGT TGGATATATT GATCCTTCCA ATGGTGAAAC TACGTATAAT
     GAAGAGCTCA GTGATATACG TGACCCAGGC AGTCCGGGGC CCATTCCCGG ACCTTACCCA ACCTATATAA CTAGGAAGGT TACCACTTTG ATGCATATTA
  29  F  S  S   H  Y  M  H   W  V  R   Q  A  P   G  K  G  L   E  W  V   G  Y  I   D  P  S  N   G  E  T   T  Y  N

                                thaI
                                fnuDII/mvnI                    scfI
             haeIII/palI        bstUI                          pstI
             sau96I             bsh1236I                       bsgI         cac8I   mnlI
             asuI              nruI                           bspMI        cac8I   ddeI  drdI
1501 CAAAAGTTCA AGGGCCGTTT CACTTTATCT CGCGACAACT CCAAAAACAC AGCATACCTG CAGATGAACA GCCTGCGTGC TGAGGACACT GCCGTCTATT
     GTTTTCAAGT TCCCGGCAAA GTGAAATAGA GCGCTGTTGA GGTTTTTGTG TCGTATGGAC GTCTACTTGT CGGACGCACG ACTCCTGTGA CGGCAGATAA
  62 Q  K  F  K   G  R  F   T  L  S   R  D  N  S   K  N  T   A  Y  L   Q  M  N  S   L  R  A   E  D  T   A  V  Y  Y

                                                                                                   sau96I
                                                                                                   haeIII/palI
                                                                                                  sau96I
                                                                                                  nlaIV
                                                                                                  hgiJII
                                                                    maeIII                        bsp1286
                                                                   bstEII                         bsp120I
                                                                 scrFI                        bmyI
                                                                 mvaI            mnlI             banII
                                           maeII                 ecoRII  bsaJI                asuI
                                          hinlI/acyI             dsaV   bseRI                 apaI
                                          ahaII/bsaHI            bstNI    esp3I                styI asuI
                                maeIII   taqI                   bsaJI hphI bsmBI        mnlI  bsaJI
          mnlI                 hphI bsrI mboII aatII         nlaIV apyI[dcm+] bsmAI  haeIII/palI eco0109I/draII
1601 ACTGTGCAAG AGGGGATTAT CGCTACAATG GTGACTGGTT CTTCGACGTC TGGGGTCAAG GAACCCTGGT CACCGTCTCC TCGGCCTCCA CCAAGGGCCC
     TGACACGTTC TCCCCTAATA GCGATGTTAC CACTGACCAA GAAGCTGCAG ACCCCAGTTC CTTGGGACCA GTGGCAGAGG AGCCGGAGGT GGTTCCCGGG
  96  C  A  R   G  D  Y   R  Y  N  G   D  W  F   F  D  V   W  G  Q  G   T  L  V   T  V  S   S  A  S  T   K  G  P
                                                            seq right is from p6G425chim2.fab2   ^
```

FIG. 41F

```
                                                                                     scrFI
                                                                                     mvaI
                                                                           scrFI
                                                                           mvaI      ecoRII
                     nlaIV                                                 ecoRII
                     hgiCI                                                 dsaV
                     banI                                                  bstNI     ecoNI
                  scrFI                                              sau96I dsaV
                  mvaI                                                  haeIII/palI  bstNI                                  hphI
                  ecoRII                                          fnu4HI     fnu4HI                               mspI
                  dsaV          hgiAI/aspHI                       bsoFI bsaJI     bslI                            hpaII
         mboII    bstNI     bseRI     bsp1286                           aciI  apyI[dcm+]                               cfr10I/bsrFI
        bpuAI     apyI[dcm+]  mnlI    bsiHKAI                    bsp1286   asuI     bsoFI                              bsaWI  tth111I/aspI
        bbsI     bsaJI     mnlI       bmyI mnlI                  bmyI nspBII bsaJI bbvI apyI[dcm+]           bslI   ageI maeIII
1701 ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT GGGGGCACAG CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG
     TAGCCAGAAG GGGGACCGTG GGAGGAGGTT CTCGTGGAGA CCCCCGTGTC GCCGGGACCC GACGGACCAG TTCCTGATGA AGGGGCTTGG CCACTGCCAC
 129  S  V  F   P  L  A  P   S  S  K   S  T  S   G  G  T  A   A  L  G   C  L  V   K  D  Y  F   P  E  P   V  T  V

                 hinPI
                  hhaI/cfoI
                 nlaIV                hgiAI/aspHI
                 narI                 bsp1286
                 kasI                 bsiHKAI      mspI
                 hinlI/acyI        cac8I           hpaII
                 hgiCI          fnu4HI            scrFI               ddeI                   fnu4HI
                 haeII          bsoFI bmyI        nciI               mnlI    pleI             bsoFI     maeIII     mnlI
                 banI           aciI  apaLI/snoI  dsaV               eco81I hinfI        ddeI        hphI     bsp1286
            ddeI ahaII/bsaHI nspBII   alw44I/snoI cauII      scfI    bsu36I/mstII/sauI mnlI bbvI    bstEII   bmyI bpmI/gsuI[dcm-]
1801 TCGTGGAACT CAGGCGCCCT GACCAGCGGC GTGCACACCT TCCCGGCTGT CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGCGTGGTG ACCGTGCCCT
     AGCACCTTGA GTCCGCGGGA CTGGTCGCCG CACGTGTGGA AGGGCCGACA GGATGTCAGG AGTCCTGAGA TGAGGGAGTC GTCGCACCAC TGGCACGGGA
 162 S  W  N  S   G  A  L   T  S  G   V  H  T  F   P  A  V   L  Q  S   S  G  L  Y   S  L  S   S  V  V   T  V  P  S

        aluI    nlaIV
      fnu4HI    hgiCI                                                         taqI           hgiJII
      bsoFI     banI                  tfiI                                    salI           bsp1286
      bbvI     bsp1286                hinfI                            styI   hincII/hindII  bmyI
   bstXI       bmyI               maeII                                bsaJI  accI           banII          maeIII
1901 CCAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA TCACAAGCCC AGCAACACCA AGGTCGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAAC
     GGTCGTCGAA CCCGTGGGTC TGGATGTAGA CGTTGCACTT AGTGTTCGGG TCGTTGTGGT TCCAGCTGTT CTTTCAACTC GGGTTTAGAA CACTGTTTTG
 196  S  S  L   G  T  Q   T  Y  I  C   N  V  N   H  K  P   S  N  T  K   V  D  K   K  V  E   P  K  S  C   D  K  T
```

FIG. 41G

```
                                                fnu4HI
                                                 bsoFI
                                                haeIII/palI
                                              mcrI
                                              eagI/xmaIII/eclXI
                                              eaeI
                                              cfrI
                                              bsiEI                                  sapI
           cac8I                              notI               rmaI                mboII
         nlaIII                               fnu4HI             maeI                earI/ksp632I                  rmaI
        nspI         bsp1286                  bsoFI    nlaIII    bfaI    tth111I/aspI                              maeI
        nspHI  aciI bmyI                      aciI aciI        aluI mnlI          taqI   aluI                      bfaI
2001 TCACACATGC CCGCCGTGCC CAGCACCAGA ACTGCTGGGC GGCCGCATGA AACAGCTAGA GGACAAGGTC GAAGAGCTAC TCTCCAAGAA CTACCACCTA
     AGTGTGTACG GGCGGCACGG GTCGTGGTCT TGACGACCCG CCGGCGTACT TTGTCGATCT CCTGTTCCAG CTTCTCGATG AGAGGTTCTT GATGGTGGAT
229  H  T  C   P  P  C  P   A  P  E   L  L  G   G  R  M  K   Q  L  E   D  K  V   E  E  L  L   S  K  N   Y  H  L
          ^junction between antibody and leucine zipper

                                                                                             scrFI
                                                  sphI                                       nciI
                                                ddeI nlaIII                                  mspI
                                               celII/espI              rmaI                  hpaII
                                               blpI/bpu1102I           maeI                  dsaV
                                             hinPI   nspI              bfaI  bsmFI           cauII
                                             hhaI/cfoI              sau96I  pleI           aciI
                 pleI      aluI             haeII    nspHI          haeIII/palI           fnu4HI
                 hinfI    hindIII           eco47III cac8I          asuI    hinfI         bsoFI
2101 GAGAATGAAG TGGCAAGACT CAAAAAGCTT GTCGGGGAGC GCTAAGCATG CGACGGCCCT AGAGTCCCTA ACGCTCGGTT GCCGCCGGGC GTTTTTTATT
     CTCTTACTTC ACCGTTCTGA GTTTTTCGAA CAGCCCCTCG CGATTCGTAC GCTGCCGGGA TCTCAGGGAT TGCGAGCCAA CGGCGGCCCG CAAAAAATAA
262  E  N  E  V   A  R  L   K  K  L   V  G  E  R   O (SEQ ID NO.60)

      tru9I                        aluI
      mseI                   taqI  hindIII                                          nlaIV
     hpaI   nlaIII          claI/bsp106 tru9I                    tru9I              hgiCI
     hincII/hindII   aluI   bspDI[dam-] mseI  aciI               mseI               banI
2201 GTTAACTCAT GTTTGACAGC TTATCATCGA TAAGCTTTAA TGCGGTAGTT TATCACAGTT AAATTGCTAA CGCAGTCAGG CACCGTGTAT GAAATCTAAC
     CAATTGAGTA CAAACTGTCG AATAGTAGCT ATTCGAAATT ACGCCATCAA ATAGTGTCAA TTTAACGATT GCGTCAGTCC GTGGCACATA CTTTAGATTG
```

FIG. 41H

```
                                             sfaNI                                        haeIII/palI
                                          scrFI                                      sau96I
                                          mvaI                                          scrFI
                                          ecoRII                                   nciI
                                          dsaV                               rsaI   mspI mnlI
                               nlaIV      bstNI                                   csp6I  hpaII
                           mnlI hgiCI    bsaJI                                 mspI     dsaV bslI
        hinPI              bsaJI      hphI apyI[dcm+]                          hpaII    cauII          ecoRV
        hhaI/cfoI   fokI    banI  maeIII   fokI  scfI                          cfr10I/bsrFI asuI    aciI
2301 AATGCGCTCA TCGTCATCCT CGGCACCGTC ACCCTGGATG CTGTAGGCAT AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT ATCGTCCATT
     TTACGCGAGT AGCAGTAGGA GCCGTGGCAG TGGGACCTAC GACATCCGTA TCCGAACCAA TACGGCCATG ACGGCCCGGA GAACGCCCTA TAGCAGGTAA

                                            hinPI
                                            hhaI/cfoI
                                         rmaI
                                         maeI
                                        nheI                                                                fnu4HI
                                     fnu4HI haeII                          hinPI         hgiAI/aspHI        bsoFI
                                     bsoFI  eco47III                       hhaI/cfoI     bsp1286      aciI  haeIII/palI
                         maeIII      bbvI bfaI                            mstI  bslI     bsiHKAI   mcrI    eaeI
           sfaNI  bsrI          cac8I  cac8I              sfaNI           aviII/fspI     bmyI      bsiEI   cfrI
2401 CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT ATATGCGTTG ATGCAATTTC TATGCGCACC CGTTCTCGGA GCACTGTCCG ACCGCTTTGG
     GGCTGTCGTA GCGGTCAGTG ATACCGCACG ACGATCGCGA TATACGCAAC TACGTTAAAG ATACGCGTGG GCAAGAGCCT CGTGACAGGC TGGCGAAACC

                                                                                       mnlI
                                                                                     sau3AI
                                                            sau3AI                   mboI/ndeII[dam-]
                                                            mboI/ndeII[dam-]         dpnI[dam+]
                                                            dpnI[dam+]               dpnII[dam-]
                                                            dpnII[dam-]              alwI[dam-]
         aciI                                            thaI                        nlaIV
        fnu4HI                                           fnuDII/mvnI                 bstYI/xhoII     hgaI
        bsoFI                                            bstUI  nlaIII               bamHI        mspI
      aciI  bsrI     cac8I           nlaIV     taqI      bsh1236I          bslI      alwI[dam-]   hpaII  sfaNI
2501 CCGCCGCCCA GTCCTGCTCG CTTCGCTACT TGGAGCCACT ATCGACTACG CGATCATGGC GACCACACCC GTCCTGTGGA TCCTCTACGC CGGACGCATC
     GGCGGCGGGT CAGGACGAGC GAAGCGATGA ACCTCGGTGA TAGCTGATGC GCTAGTACCG CTGGTGTGGG CAGGACACCT AGGAGATGCG GCCTGCGTAG
```

FIG. 41I

```
                  hinPI
                  hhaI/cfoI
                 nlaIV
                 narI                    hinPI
                 kasI                    hhaI/cfoI
                 hinlI/acyI              nlaIV                                  hgiJII
      mspI       hgiCI                   narI                                   bsp1286
      hpaII      haeII                   kasI                                   bmyI
     naeI      mspI                      hinlI/acyI                             banII
     cfr10I/bsrFI banI                   hgiCI                            sau3AI cac8I            rcaI  hinPI
     cac8I    sgrAI                      haeII                            mboI/ndeII[dam-]    hgiJII    haeII
    haeIII/palI hpaII                   banI                             dpnI[dam+]          bsp1286   eco47III
   eaeI      hphI ahaII/bsaHI           ahaII/bsaHI                      dpnII[dam-]         bmyI bspHI hhaI/cfoI
   cfrI  sfaNI cfr10I/bsrFI    aciI   cac8I                  hphI       mboII[dam-]         banII nlaIII
2601 GTGGCCGGCA TCACCGGCGC CACAGGTGCG GTTGCTGGCG CCTATATCGC CGACATCACC GATGGGGAAG ATCGGGCTCG CCACTTCGGG CTCATGAGCG
     CACCGGCCGT AGTGGCCGCG GTGTCCACGC CAACGACCGC GGATATAGCG GCTGTAGTGG CTACCCCTTC TAGCCCGAGC GGTGAAGCCC GAGTACTCGC

                                     scrFI
                                     nciI
                                     mspI            hinPI
                                     hpaII           hhaI/cfoI
                                dsaI dsaV            nlaIV
                                bslI cauII           narI
                           sau96I   haeIII/palI      kasI                              fnu4HI
                           nlaIV  eaeI               hinlI/acyI                        bsoFI hgiAI/aspHI
                           haeIII/palI               hgiCI                             aciI  bsp1286
                           asuI bsaJI bsaJI          haeII                        fnu4HI   bsiHKAI
                          ecoO109I/draII             banI                         bsoFI    bmyI
                       cac8I bslI cfrI    bsmFI     ahaII/bsaHI    cac8I      bslI aciI  aciI        haeIII/palI
2701 CTTGTTTCGG CGTGGGTATG GTGGCAGGCC CCGTGGCCGG GGGACTGTTG GGCGCCATCT CCTTGCACGC ACCATTCCTT GCGGCGGCGG TGCTCAACGG
     GAACAAAGCC GCACCCATAC CACCGTCCGG GGCACCGGCC CCCTGACAAC CCGCGGTAGA GGAACGTGCG TGGTAAGGAA CGCCGCCGCC ACGAGTTGCC

                                                                                                    mspI
                      fnu4HI                                                                        hpaII
                      bsoFI   ecoNI      pleI                                                       bsaWI
    mnlI  bslI   bsrI bbvI    bslI       hinfI            hgaI      sfaNI                  bsrI  aluI bslI
2801 CCTCAACCTA CTACTGGGCT GCTTCCTAAT GCAGGAGTCG CATAAGGGAG AGCGTCGTCC GATGCCCTTG AGAGCCTTCA ACCCAGTCAG CTCCTTCCGG
     GGAGTTGGAT GATGACCCGA CGAAGGATTA CGTCCTCAGC GTATTCCCTC TCGCAGCAGG CTACGGGAAC TCTCGGAAGT TGGGTCAGTC GAGGAAGGCC
```

FIG. 41J

```
                                                                                   fnu4HI
                                                                                mspI  hinPI
     aciI                                                                      naeI  haeII
    thaI                                                                       cfr10I/bsrFI
    fnuDII/mvnI                                                                cac8I eco47III
    bstUI   nlaIII                                                         nlaIV   bsoFI
    bsh1236I               aciI             mboII                          hgiCI   bbvI
   hinPI   bcgI           fnu4HI           bpuAI                           banI hpaII hhaI/cfoI         mnlI
   hhaI/cfoI              bsoFI            bbsI          nlaIII
2901 TGGGCGCGGG GCATGACTAT CGTCGCCGCA CTTATGACTG TCTTCTTTAT CATGCAACTC GTAGGACAGG TGCCGGCAGC GCTCTGGGTC ATTTTCGGCG
     ACCCGCGCCC CGTACTGATA GCAGCGGCGT GAATACTGAC AGAAGAAATA GTACGTTGAG CATCCTGTCC ACGGCCGTCG CGAGACCCAG TAAAAGCCGC

                   thaI
                   fnuDII/mvnI                                                                    sau96I
                   bstUI        haeIII/palI                                                       nlaIV
    aciI           bsh1236I  sau3AI                                                               avaII
  sau96I          hinPI      mboI/ndeII[dam-]                                                     asuI
  avaII           hhaI/cfoI  dpnI[dam+]       aciI       tfiI                                  bsrI    aciI
  asuI        bpmI/gsuI[dcm-] dpnII[dam-]    cac8I       hinfI    cac8I mnlI                 maeIII  bsmFI
3001 AGGACCGCTT TCGCTGGAGC GCGACGATGA TCGGCCTGTC GCTTGCGGTA TTCGGAATCT TGCACGCCCT CGCTCAAGCC TTCGTCACTG GTCCCGCCAC
     TCCTGGCGAA AGCGACCTCG CGCTGCTACT AGCCGGACAG CGAACGCCAT AAGCCTTAGA ACGTGCGGGA GCGAGTTCGG AAGCAGTGAC CAGGGCGGTG

                                            mcrI
                                            eagI/xmaIII/eclXI
                                            eaeI    hinPI
                                            cfrI    hhaI/cfoI                           thaI
                                   mspI     bsiEI  thaI                               hgaI
                                  naeI     fnu4HI  fnuDII/mvnI                      thaI  fnuDII/mvnI
                                  cfr10I/bsrFI     bstUI                            fnuDII/mvnI
                        haeIII/palI hpaII  bsoFI   bsh1236I                         bstUI bstUI
   maeII               haeI       cac8I    aciI  hgaI                               bsh1236I mnlI      haeI
  psp1406I          cac8I         bglI nlaIII haeIII/palI      maeII   cac8I    nruI    bsh1236I fokI haeIII/palI
3101 CAAACGTTTC GGCGAGAAGC AGGCCATTAT CGCCGGCATG GCGGCCGACG CGCTGGGCTA CGTCTTGCTG GCGTTCGCGA CGCGAGGCTG GATGGCCTTC
     GTTTGCAAAG CCGCTCTTCG TCCGGTAATA GCGGCCGTAC CGCCGGCTGC GCGACCCGAT GCAGAACGAC CGCAAGCGCT GCGCTCCGAC CTACCGGAAG
```

FIG. 41K

```
                                                                  bspMI
                                               thaI              scrFI
                              fnu4HI           fnuDII/mvnI       mvaI
                              bsoFI            bstUI             ecoRII
          mboII               aciI         cac8I      haeI       dsaV
        tfiI               mspI   mslI   sfaNI  bsh1236I  haeIII/palI bstNI
        hinfI              hpaII sfaNI  fokI   aciI   cac8I  nlaIII  apyI[dcm+]            bsmFI aluI    alwI[dam-]
3201 CCCATTATGA TTCTTCTCGC TTCCGGCGGC ATCGGGATGC CCGCGTTGCA GGCCATGCTG TCCAGGCAGG TAGATGACGA CCATCAGGGA CAGCTTCAAG
     GGGTAATACT AAGAAGAGCG AAGGCCGCCG TAGCCCTACG GGCGCAACGT CCGGTACGAC AGGTCCGTCC ATCTACTGCT GGTAGTCCCT GTCGAAGTTC

        fnu4HI
        bsoFI
        aciI
       thaI                               sau96I
       fnuDII/mvnI                        avaII
       bstUI                           bsrI        sau3AI               mnlI
     cac8I                          sau3AI asuI    mboI/ndeII[dam-]     bsaJI    hgiAI/aspHI
  sau3AI bsh1236I                   mboI/ndeII[dam-]                  aciI       bsp1286
  mboI/ndeII[dam-]                  dpnI[dam+] nspBII    maeIII       fnu4HI     bsiHKAI
  dpnI[dam+]                        dpnII[dam-]    dpnI[dam+]         bsoFI      bmyI
  dpnII[dam-]                     taqI[dam-]    aciI dpnII[dam-]      bglI    cac8I   nlaIII        nlaIII
3301 GATCGCTCGC GGCTCTTACC AGCCTAACTT CGATCACTGG ACCGCTGATC GTCACGGCGA TTTATGCCGC CTCGGCGAGC ACATGGAACG GGTTGGCATG
     CTAGCGAGCG CCGAGAATGG TCGGATTGAA GCTAGTGACC TGGCGACTAG CAGTGCCGCT AAATACGGCG GAGCCGCTCG TGTACCTTGC CCAACCGTAC

          fnu4HI
          bsoFI
        hinPI
        hhaI/cfoI                                                haeIII/palI
        nlaIV                                                   sau96I                         fnu4HI
        narI                                                   scrFI                           bsoFI
        kasI                                    thaI           nciI                            aciI
        hinlI/acyI                    thaI      fnuDII/mvnI    mspI                          mspI      mnlI
        hgiCI                         fnuDII/mvnI              hpaII                         hpaII nlaIV
        haeII                         bstUI     bstUI          dsaV                         naeI   hgiCI
        banI aciI                     bsh1236I  bsh1236I  nlaIV  asuI    taqI               cfr10I/bsrFI
        ahaII/bsaHI              mnlI aciI   hgaI aciI  nlaIII  cauII  mnlI                cac8I  banI
3401 GATTGTAGGC GCCGCCCTAT ACCTTGTCTG CCTCCCCGCG TTGCGTCGCG GTGCATGGAG CCGGGCCACC TCGACCTGAA TGGAAGCCGG CGGCACCTCG
     CTAACATCCG CGGCGGGATA TGGAACAGAC GGAGGGGCGC AACGCAGCGC CACGTACCTC GGCCCGGTGG AGCTGGACTT ACCTTCGGCC GCCGTGGAGC
```

FIG. 41L

```
                                                                           hinPI                             hgaI
                                                                           hhaI/cfoI                        thaI aciI
        hphI                                                              mstI     pflMI                    fnuDII/mvnI
      tfiI         pflMI                                                  aviII/fspI   styI                 bstUI
      hinfI        bslI      nlaIV                aciI         bsmI          bslI  bsaJI                    bsh1236I
3501 CTAACGGATT CACCACTCCA AGAATTGGAG CCAATCAATT CTTGCGGAGA ACTGTGAATG CGCAAACCAA CCCTTGGCAG AACATATCCA TCGCGTCCGC
     GATTGCCTAA GTGGTGAGGT TCTTAACCTC GGTTAGTTAA GAACGCCTCT TGACACTTAC GCGTTTGGTT GGGAACCGTC TTGTATAGGT AGCGCAGGCG

                                                    haeIII/palI
                                                   mscI/balI
                                                   haeI
                                                  scrFI
                                                  mvaI dsaI                                                mspI
                                                  ecoRII                                              hpaII
                                                  dsaV                                               scrFI
                                                  bstNI                                                    nciI
               fnu4HI                             bslI bsaJI        sau3AI                                 dsaV
              thaI hinPI                          apyI[dcm+]        mboI/ndeII[dam-]                    sau96I
           fnu4HI bsoFI                         sau96I          dpnI[dam+]                    nlaIV
           bsoFI fnuDII/mvnI                    avaII      hinPI dpnII[dam-]                  avaII           cac8I
       fnu4HI    bstUI                          asuI eaeI  hhaI/cfoI  hgiAI/aspHI              asuI      rmaI
       bsoFI  cac8I   hhaI/cfoI    fnu4HI     ppuMI      mstI nlaIII bsp1286                 ppuMI      maeI
       bbvI aciI bsh1236I   avaI   bsoFI      nlaIV cfrI       aviII/fspI  bsiHKAI              eco0109I/draII
  bpmI/gsuI[dcm-] aciI  sfaNI      bbvI       eco0109I/draII  mslI    bmyI             mnlI cauII·bfaI    aciI
3601 CATCTCCAGC AGCCGCACGC GGCGCATCTC GGGCAGCGTT GGGTCCTGGC CACGGGTGCG CATGATCGTG CTCCTGTCGT TGAGGACCCG GCTAGGCTGG
     GTAGAGGTCG TCGGCGTGCG CCGCGTAGAG CCCGTCGCAA CCCAGGACCG GTGCCCACGC GTACTAGCAC GAGGACAGCA ACTCCTGGGC CGATCCGACC

                                                                    fnu4HI
                                             cac8I                  bsoFI
                                           thaI                     bbvI
                                  hphI     fnuDII/mvnI            fnu4HI
                              tfiI         bstUI                  bsoFI
                bsrI          hinfI        bsh1236I  maeII        bbvI       maeII      ddeI        nlaIII
3701 CGGGGTTGCC TTACTGGTTA GCAGAATGAA TCACCGATAC GCGAGCGAAC GTGAAGCGAC TGCTGCTGCA AAACGTCTGC GACCTGAGCA ACAACATGAA
     GCCCCAACGG AATGACCAAT CGTCTTACTT AGTGGCTATG CGCTCGCTTG CACTTCGCTG ACGACGACGT TTTGCAGACG CTGGACTCGT TGTTGTACTT
```

FIG. 41M

```
                                                                                  sau3AI
                                                                                  mboI/ndeII[dam-]
                                                                                  mamI[dam-]
                                                                                  dpnI[dam+]
                                                                                  dpnII[dam-]
                                                                                bstYI/xhoII
                                                                                alwI[dam-]
                                                                              mspI
                                                                              hpaII
                                             aciI                            mroI bsaBI[dam-]       fnu4HI
                                            thaI                             bspMII                 bsoFI
        mboII                               fnuDII/mvnI hinPI                bspEI[dam-]            bbvI
       bpuAI                                bstUI       hhaI/cfoI            bsaWI     sfaNI     sfaNI
       bbsI                                 bsh1236I   haeII     mslI        accIII[dam-]       fokI    cac8I
3801 TGGTCTTCGG TTTCCGTGTT TCGTAAAGTC TGGAAACGCG GAAGTCAGCG CCCTGCACCA TTATGTTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC
     ACCAGAAGCC AAAGGCACAA AGCATTTCAG ACCTTTGCGC CTTCAGTCGC GGGACGTGGT AATACAAGGC CTAGACGTAG CGTCCTACGA CGACCGATGG

                                                                             aciI
                                        cac8I                            bsmFI     fokI
                                      hinPI                             sau96I    sfaNI
                                      hhaI/cfoI                         nlaIV  aciI
                             tru9I  haeII                               avaII fnu4HI           bsrI
                             mseI   eco47III          ddeI              asuI  bsoFI         aciI             mnlI
3901 CTGTGGAACA CCTACATCTG TATTAACGAA GCGCTGGCAT TGACCCTGAG TGATTTTTCT CTGGTCCCGC CGCATCCATA CCGCCAGTTG TTTACCCTCA
     GACACCTTGT GGATGTAGAC ATAATTGCTT CGCGACCGTA ACTGGGACTC ACTAAAAAGA GACCAGGGCG GCGTAGGTAT GGCGGTCAAC AAATGGGAGT

                        nspI
                    scrFI
                    nciI
                    mspI
            bsrI    hpaII
            bslI    dsaV nlaIII                                mnlI
       maeII        cauII                                    fokI
      psp1406I  maeIII  nspHI            maeIII           sfaNI                                  nlaIII    apoI   bslI
4001 CAACGTTCCA GTAACCGGGC ATGTTCATCA TCAGTAACCC GTATCGTGAG CATCCTCTCT CGTTTCATCG GTATCATTAC CCCCATGAAC AGAAATTCCC
     GTTGCAAGGT CATTGGCCCG TACAAGTAGT AGTCATTGGG CATAGCACTC GTAGGAGAGA GCAAAGTAGC CATAGTAATG GGGGTACTTG TCTTTAAGGG
```

FIG. 41N

```
                                                         cac8I
                                                        sau96I
                                                 tru9I  haeIII/palI                          tru9I
           sfaNI                                 mseI   asuI                                 mseI      bpmI/gsuI[dcm-]
       mnlI       maeIII                   aciI bslI  nlaIII aciI                            mseI      bpmI/gsuI[dcm-]
4101 CCTTACACGG AGGCATCAAG TGACCAAACA GGAAAAAACC GCCCTTAACA TGGCCCGCTT TATCAGAAGC CAGACATTAA CGCTTCTGGA GAAACTCAAC
     GGAATGTGCC TCCGTAGTTC ACTGGTTTGT CCTTTTTTGG CGGGAATTGT ACCGGGCGAA ATAGTCTTCG GTCTGTAATT GCGAAGACCT CTTTGAGTTG

                                                                                fnu4HI   thaI
                                                                                bsoFI    fnuDII/mvnI
                                                                               aluI      bstUI
                                                                              pvuII     hinPI
       aciI                                                                   nspBII    hhaI/cfoI
      thaI                                                                   fnu4HI    thaI
      fnuDII/mvnI               xmnI                                         bsoFI     fnuDII/mvnI
      bstUI                     tfiI                                         bcgI      bstUI
      bsh1236I                  hinfI                                        bbvI   mnlI bsh1236I
  aluI hgaI  fokI               asp700         mslI       aluI      aciI  bbvI   bsh1236I  hphI      hphI
4201 GAGCTGGACG CGGATGAACA GGCAGACATC TGTGAATCGC TTCACGACCA CGCTGATGAG CTTTACCGCA GCTGCCTCGC GCGTTTCGGT GATGACGGTG
     CTCGACCTGC GCCTACTTGT CCGTCTGTAG ACACTTAGCG AAGTGCTGGT GCGACTACTC GAAATGGCGT CGACGGAGCG CGCAAAGCCA CTACTGCCAC

                         esp3I
                         bsmBI
                         bsmAI
                       mspI                                  scrFI                      hgaI
                 fnu4HI  hpaII                               nciI                      thaI
                 bsoFI  scrFI                                mspI                      fnuDII/mvnI
                 bbvI   nciI                                 hpaII                     bstUI  aciI
               nlaIII   dsaV                              sfaNI                        bsh1236I
              nspI      cauII          aluI              fokI dsaV                    hinPI nspBII
    mnlI      nspHI aluI bslI       maeIII             aciI   cauII     drdI          hhaI/cfoI          aciI
4301 AAAACCTCTG ACACATGCAG CTCCCGGAGA CGGTCACAGC TTGTCTGTAA GCGGATGCCG GGAGCAGACA AGCCCGTCAG GGCGCGTCAG CGGGTGTTGG
     TTTTGGAGAC TGTGTACGTC GAGGGCCTCT GCCAGTGTCG AACAGACATT CGCCTACGGC CCTCGTCTGT TCGGGCAGTC CCGCGCAGTC GCCCACAACC
```

FIG. 41O

```
                                                                                                           hgiAI/aspHI
                   fnu4HI                                                                                  bsp1286
                   bsoFI              maeII                                     sfaNI                      bsiHKAI
                   bbvI           maeIII                                     fnu4HI                 ddeI   bmyI  ndeI
                 hinPI  nlaIII bsrI bsaAI                bst1107I   tru9I    bsoFI               rsaI      apaLI/snoI
                 hhaI/cfoI  tth111I/aspI          aciI   accI bsrI  mseI     aciI                csp6I     alw44I/snoI
4401 CGGGTGTCGG GGCGCAGCCA TGACCCAGTC ACGTAGCGAT AGCGGAGTGT ATACTGGCTT AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC
     GCCCACAGCC CCGCGTCGGT ACTGGGTCAG TGCATCGCTA TCGCCTCACA TATGACCGAA TTGATACGCC GTAGTCTCGT CTAACATGAC TCTCACGTGG

                                                                  mboII
                                                                 earI/ksp632I                     hinPI
                                                                sapI                              hhaI/cfoI
                                                              hinPI                            fnu4HI
                                                      sfaNI   hhaI/cfoI                  pleI  bsoFI    mcrI
         aciI          aciI    sfaNI                aciI     haeII     aciI  mnlI        hinfI bbvI     bsiEI
4501 ATATGCGGTG TGAAATACCG CACAGATGCG TAAGGAGAAA ATACCGCATC AGGCGCTCTT CCGCTTCCTC GCTCACTGAC TCGCTGCGCT CGGTCGTTCG
     TATACGCCAC ACTTTATGGC GTGTCTACGC ATTCCTCTTT TATGGCGTAG TCCGCGAGAA GGCGAAGGAG CGAGTGACTG AGCGACGCGA GCCAGCAAGC

        fnu4HI
        bsoFI
        aciI                                                                              nlaIII           bslI
     fnu4HI     aciI                                                                     nspI             cac8I
     bsoFI   bsrBI                                            tfiI                       nspHI           haeIII/palI
     bbvI  cac8I        aluI           aciI                   hinfI                      aflIII         haeI
4601 GCTGCGGCGA GCGGTATCAG CTCACTCAAA GGCGGTAATA CGGTTATCCA CAGAATCAGG GGATAACGCA GGAAAGAACA TGTGAGCAAA AGGCCAGCAA
     CGACGCCGCT CGCCATAGTC GAGTGAGTTT CCGCCATTAT GCCAATAGGT GTCTTAGTCC CCTATTGCGT CCTTTCTTGT ACACTCGTTT TCCGGTCGTT

         scrFI          thaI
         mvaI                 fnuDII/mvnI
         ecoRII         bstUI
         dsaV           bsh1236I
         bstNI   bslI       aciI
         apyI[dcm+]         fnu4HI                                                         hgaI
       haeIII/palI          bsoFI  cac8I                   aciI                           drdI
      haeI  nlaIV          haeIII/palI                nlaIV           sfaNI       taqI             mnlI
4701 AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT TCCATAGGCT CCGCCCCCCT GACGAGCATC ACAAAAATCG ACGCTCAAGT CAGAGGTGGC
     TTCCGGTCCT TGGCATTTTT CCGGCGCAAC GACCGCAAAA AGGTATCCGA GGCGGGGGGA CTGCTCGTAG TGTTTTTAGC TGCGAGTTCA GTCTCCACCG
```

FIG. 41P

```
                                        scrFI
                           scrFI   mvaI
                           mvaI         ecoRII
                           ecoRII  dsaV                                      bslI
                           dsaV    bstNI              hinPI                        aciI     mspI
                           bstNI        apyI[dcm+]     bssSI                           fnu4HI   hpaII
                           apyI[dcm+]  bsaJI    aluI mnlI   hhaI/cfoI                  bsoFI   bsaWI        aciI
4801 GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT ACCTGTCCGC
     CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAAGGGGG ACCTTCGAGG GAGCACGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA TGGACAGGCG

                                                                                                   hgiAI/aspHI
                                                                                                   bsp1286
                                                                                                   bsiHKAI
                        hinPI                                                                      bmyI
                        hhaI/cfoI                                                                  apaLI/snoI
                       haeII        aluI      scfI        ddeI                          aluI       alw44I/snoI
4901 CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA
     GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC ACACGTGCTT

                                                                                               alwNI[dcm-]
                    fnu4HI                                       mspI                         fnu4HI
                    bsoFI                                        hpaII                        bsoFI
                  nspBII             maeIII                      scrFI                     fnu4HI
                  aciI  hinPI      mspI                          nciI                      bsoFI
               mcrI bbvI          bsaWI              pleI        dsaV                      bbvI               maeIII
               bsiEI    hhaI/cfoI hpaII              hinfI       cauII                 bsrI    bbvI    bsrI
5001 CCCCCCGTTC AGCCCGACCG CTGCGCCTTA TCCGGTAACT ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA GCCACTGGTA
     GGGGGGCAAG TCGGGCTGGC GACGCGGAAT AGGCCATTGA TAGCAGAACT CAGGTTGGGC CATTCTGTGC TGAATAGCGG TGACCGTCGT CGGTGACCAT

                                                                 bslI           rmaI
                                                               haeIII/palI      maeI                 hinPI
                 mnlI        aciI    scfI                      haeI             bfaI                 hhaI/cfoI
5101 ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC
     TGTCCTAATC GTCTCGCTCC ATACATCCGC CACGATGTCT CAAGAACTTC ACCACCGGAT TGATGCCGAT GTGATCTTCC TGTCATAAAC CATAGACGCG
```

FIG. 41Q

```
                                                  mspI
                                                  hpaII
                                               sau3AI
                                               mboI/ndeII[dam-]                                    fnu4HI
                                               dpnI[dam+]                                          bsoFI
                  maeIII                       dpnII[dam-]          nspBII                         bbvI
        eco57I bsrI                      aluI  alwI[dam-]          aciI      aciI                 cac8I
5201 TCTGCTGAAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTTGTTTG CAAGCAGCAG
     AGACGACTTC GGTCAATGGA AGCCTTTTTC TCAACCATCG AGAACTAGGC CGTTTGTTTG GTGGCGACCA TCGCCACCAA AAAAACAAAC GTTCGTCGTC

                                        sau3AI
                                  sau3AI  mboI/ndeII[dam-]
                                  mboI/ndeII[dam-]
         hinPI          sau3AI   mboII[dam-] dpnI[dam+]
         hhaI/cfoI      mboI/ndeII[dam-]     dpnII[dam-]
        thaI            dpnI[dam+]   dpnI[dam+]
        fnuDII/mvnI     dpnII[dam-]  dpnII[dam-]                                    tru9I          nlaIII
        bstUI          bstYI/xhoII   alwI[dam-]                                     mseI           rcaI
        bsh1236I       alwI[dam-]  bstYI/xhoII                    hgaI ddeI       maeII          bspHI
5301 ATTACGCGCA GAAAAAAAGG ATCTCAAGAA GATCCTTTGA TCTTTTCTAC GGGGTCTGAC GCTCAGTGGA ACGAAAACTC ACGTTAAGGG ATTTTGGTCA
     TAATGCGCGT CTTTTTTTCC TAGAGTTCTT CTAGGAAACT AGAAAAGATG CCCCAGACTG CGAGTCACCT TGCTTTTGAG TGCAATTCCC TAAAACCAGT

                              sau3AI
                              mboI/ndeII[dam-]
                           rmaI
                        hphI   dpnI[dam+]
                     mboII[dam-]
                   sau3AI    maeI       tru9I
                   mboI/ndeII[dam-]     mseI
                   dpnI[dam+]   dpnII[dam-]
                   dpnII[dam-]  alwI[dam-]    tru9I          tru9I
                  bstYI/xhoII  bstYI/xhoII    mseI           mseI
                  alwI[dam-] bfaI      ahaIII/draI          ahaIII/draI                              maeIII
5401 TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TTAAAAATGA AGTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA
     ACTCTAATAG TTTTTCCTAG AAGTGGATCT AGGAAAATTT AATTTTTACT TCAAAATTTA GTTAGATTTC ATATATACTC ATTTGAACCA GACTGTCAAT

                     nlaIV            sau3AI
                     hgiCI            mboI/ndeII[dam-]                  pleI
           tru9I     banI             dpnI[dam+]                        hinfI
           mseI      mnlI       ddeI  dpnII[dam-]       fokI           ahdI/eam1105I                    mnlI
5501 CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT CATCCATAGT TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG
     GGTTACGAAT TAGTCACTCC GTGGATAGAG TCGCTAGACA GATAAAGCAA GTAGGTATCA ACGGACTGAG GGGCAGCACA TCTATTGATG CTATGCCCTC
```

FIG. 41R

```
                                        bsmAI
                                        bsaI
                    bsrI                thaI                bpmI/gsuI[dcm-]
                 sau96I    fnu4HI       fnuDII/mvnI      mspI                                  mspI
                 nlaIV     bsoFI        bstUI            hpaII                                 hpaII   haeIII/palI
                 haeIII/palI bsrDI      bsh1236I         cfr10I/bsrFI                          bglI    sau96I hinPI
                 asuI      bbvI         aciI          hphI  nlaIV                      cac8I       asuI   hhaI/cfoI
5601 GGCTTACCAT CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCACGCTC ACCGGCTCCA GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC
     CCGAATGGTA GACCGGGGTC ACGACGTTAC TATGGCGCTC TGGGTGCGAG TGGCCGAGGT CTAAATAGTC GTTATTTGGT CGGTCGGCCT TCCCGGCTCG

                                                 scrFI
                                                 nciI
                                                 mspI                                              maeII
                                                 hpaII    rmaI                                  hinPI
          sau96I                                 dsaV     maeI                                  hhaI/cfoI
          avaII                 mnlI    bsrI     mseI     cauII    bfaI                tru9I    mstI psp1406I
          asuI                aciI    fokI       aseI/asnI/vspI    aluI                bsrI mseI     aviII/fspI
5701 GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT
     CGTCTTCACC AGGACGTTGA AATAGGCGGA GGTAGGTCAG ATAATTAACA ACGGCCCTTC GATCTCATTC ATCAAGCGGT CAATTATCAA ACGCGTTGCA

               cac8I
              scfI                                                                          sau3AI
              pstI                                                                          mboI/ndeII[dam-]
             fnu4HI                                                          nlaIV      sau3AI          dpnI[dam+]
             bsoFI                                                           mspI       mboI/ndeII[dam-]  dpnII[dam-]
             bbvI    mslI                                                    bsaWI      dpnI[dam+]      nlaIII    nlaIII
         bsrDI bsgI  sfaNI      maeIII                                      aluI hpaII    dpnII[dam-] maeIII  alwI[dam-]
5801 TGTTGCCATT GCTGCAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTCATTCAG CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC
     ACAACGGTAA CGACGTCCGT AGCACCACAG TGCGAGCAGC AAACCATACC GAAGTAAGTC GAGGCCAAGG GTTGCTAGTT CCGCTCAATG TACTAGGGGG

                                    sau3AI
                                    mboI/ndeII[dam-]          aciI
                                    dpnI[dam+]                fnu4HI
                                 mnlI dpnII[dam-]             bsoFI
                               sau96I pvuI/bspCI              haeIII/palI                    fnu4HI
                               avaII  mcrI                    eaeI              nlaIII       bsoFI
                    aciI   aluI      asuI   bsiEI             cfrI              mslI         bbvI
5901 ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC GGTCCTCCGA TCGTTGTCAG AAGTAAGTTG GCCGCAGTGT TATCACTCAT GGTTATGGCA GCACTGCATA
     TACAACACGT TTTTTCGCCA ATCGAGGAAG CCAGGAGGCT AGCAACAGTC TTCATTCAAC CGGCGTCACA ATAGTGAGTA CCAATACCGT CGTGACGTAT
```

FIG. 41S

```
                                                                                          mcrI
                                                                                          bsiEI
                                                                                          bcgI
                                                           rsaI                       fnu4HI
                                                    bsrI   scaI                       bsoFI
                         fokI
                     nlaIII          sfaNI       maeIII hphI csp6I          ddeI          aciI
6001 ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC
     TAAGAGAATG ACAGTACGGT AGGCATTCTA CGAAAAGACA CTGACCACTC ATGAGTTGGT TCAGTAAGAC TCTTATCACA TACGCCGCTG GCTCAACGAG

          hgaI
         hinlI/acyI
         ahaII/bsaHI
       mspI                     hinPI
       hpaII                    hhaI/cfoI                                                                 sau3AI
      scrFI                    thaI                                                                        mboI/ndeII[dam-]
      nciI                     fnuDII/mvnI                        hgiAI/aspHI                              dpnI[dam+]
      dsaV                     bstUI                              bsp1286         maeII                    dpnII[dam-]
      cauII hincII/hindII      bsh1236I             tru9I         bsiHKAI        psp1406I                  bstYI/xhoII
                               aciI                 mseI          bmyI          xmnI                       alwI[dam-]
                                                 ahaIII/draI                    asp700   mboII
6101 TTGCCCGGCG TCAACACGGG ATAATACCGC GCCACATAGC AGAACTTTAA AAGTGCTCAT CATTGGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC
     AACGGGCCGC AGTTGTGCCC TATTATGGCG CGGTGTATCG TCTTGAAATT TTCACGAGTA GTAACCTTTT GCAAGAAGCC CCGCTTTTGA GAGTTCCTAG

                bsrI                      hgiAI/aspHI
             sau3AI   taqI                bsp1286          eco57I
             mboI/ndeII[dam-]             bsiHKAI         mboII[dam-]
             dpnI[dam+]                   bmyI          sau3AI   sfaNI
             dpnII[dam-]                  apaLI/snoI    mboI/ndeII[dam-]
      nspBII alwI[dam-]                   alw44I/snoI   dpnI[dam+]
      aciI  bstYI/xhoII     maeIII     bssSI            dpnII[dam-]           hphI         hphI
6201 TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCAACTG ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCAAAAACAG
     AATGGCGACA ACTCTAGGTC AAGCTACATT GGGTGAGCAC GTGGGTTGAC TAGAAGTCGT AGAAAATGAA AGTGGTCGCA AAGACCCACT CGTTTTTGTC

            aciI
           fnu4HI                                                 mboII
           bsoFI                  mslI                        earI/ksp632I   sspI
6301 GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA
     CTTCCGTTTT ACGGCGTTTT TTCCCTTATT CCCGCTGTGC CTTTACAACT TATGAGTATG AGAAGGAAAA AGTTATAATA ACTTCGTAAA TAGTCCCAAT
```

FIG. 41T

```
                                                                                                  hinPI
                                                                                                 thaI
                                                                                                 fnuDII/mvnI
                                                                                                 bstUI                                  maeII
          nlaIII                                                                                 bsh1236I                               hinlI/acyI
         rcaI                                                                                   aciI                                   ahaII/bsaHI
         bspHI  aciI                                                                          nlaIV  hhaI/cfoI                         aatII ddeI
       bsmAI  bsrBI
6401 TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA TAGGGGTTCC GCGCACATTT CCCCGAAAAG TGCCACCTGA CGTCTAAGAA
     AACAGAGTAC TCGCCTATGT ATAAACTTAC ATAAATCTTT TTATTTGTTT ATCCCCAAGG CGCGTGTAAA GGGGCTTTTC ACGGTGGACT GCAGATTCTT

                                                                 sau96I
                                                                 haeIII/palI
                                                                 asuI       mboII
                 nlaIII                                         eco0109I/draII
                rcaI    tru9I                                  mnlI        bpuAI
                bspHI   mseI                                  bssSI        bbsI
6501 ACCATTATTA TCATGACATT AACCTATAAA AATAGGCGTA TCACGAGGCC CTTTCGTCTT CAA  (SEQ ID NO.61)
     TGGTAATAAT AGTACTGTAA TTGGATATTT TTATCCGCAT AGTGCTCCGG GAAAGCAGAA GTT
```

FIG. 41U

```
>length: 6563

aatII(GACGTC):              1645 6489
acc65I(GGTACC):             403 823
accI(GTMKAC):               1093 1963 4449
accIII(TCCGGA):             3867[dam-]
aciI(CCGC):                 178 542 805 877 1340 1750 1826 2011 2039 2043 2182 2242 2384 2492 2501 2504
                            2628 2781 2784 2787 2906 2926 3005 3045 3094 3141 3226 3241 3309 3342 3367 3412
                            3436 3448 3490 3544 3597 3613 3619 3700 3838 3967 3970 3981 4139 4155 4210 4266
                            4351 4390 4400 4442 4467 4505 4518 4544 4561 4604 4611 4632 4723 4751 4878 4897
                            5018 5128 5263 5272 5634 5725 5916 5962 6083 6127 6204 6313 6412 6459
acyI                        see hinlI
aflIII(ACRYGT):             1307 4678
ageI(ACCGGT):               1788
ahaII/bsaHI(GRCGYC):        1645 1813 2616 2637 2751 3408 6107 6489
ahaIII/draI(TTTAAA):        5435 5454 6146
ahdI/eam1105I(GACNNNNNGTC): 346 5566
aluI(AGCT):                 72 121 252 320 398 532 589 648 1126 1144 1167 1325 1386 1906 2054 2075 2126
                            2218 2233 2889 3292 4202 4259 4270 4319 4338 4619 4845 4935 4981 5238 5759 5859
                            5922
alw44I/snoI(GTGCAC):        1831 4494 4992 6238
alwI[dam-](GGATC):          412 413 712 713 1171 1471 2578 2579 3300 3870 5245 5319 5331 5416 5429 5893
                            6196 6214
alwNI[dcm-](CAGNNNCTG):     1117 1385 5089
apaI(GGGCCC):               1695
apaLI/snoI(GTGCAC):         1831 4494 4992 6238
apoI(RAATTY):               1 391 4093
apyI[dcm+](CCWGG):          640 999 1347 1357 1449 1665 1713 1755 1764 2333 3262 3645 4705 4826 4839
aseI/asnI/vspI(ATTAAT):     5742
asnI                        see aseI
asp700(GAANNNNTTC):         905 930 4234 6166
asp718(GGTACC):             403 823
aspHI                       see hgiAI
aspI                        see tth111I
asuI(GGNCC):                1119 1195 1425 1434 1446 1512 1695 1696 1752 2155 2375 2727 3002 3090 3339 3463
```

FIG. 41V

Stop Template Primer

SL.97.2 5' CAT GGT ATA GGT TAA ACT TAT TTA CAC 3' (SEQ ID NO.63)

NNS Randomization Primer

SL.97.3 5' CAT GGT ATA GGT NNS ACT TAT TTA CAC 3' (SEQ ID NO.64)

FIG. 42

Randomization of Position N35 of Variable Light Chain CDR-1 Amino Acid Frequency

Phage Display (NNS Codon Library) Sort #3

Amino Acid	Frequency	% Total	IC50 (nM)
Asparagine (wt)	1	5.6	4.9
Glycine	6	16.6	3.1
Aspartic Acid	3	16.6	3.1
Glutamic Acid	4	22.2	0.1
Alanine	2	5.6	0.2
Lysine	1	5.6	ND
Serine	1	1.9	ND

FIG. 43A

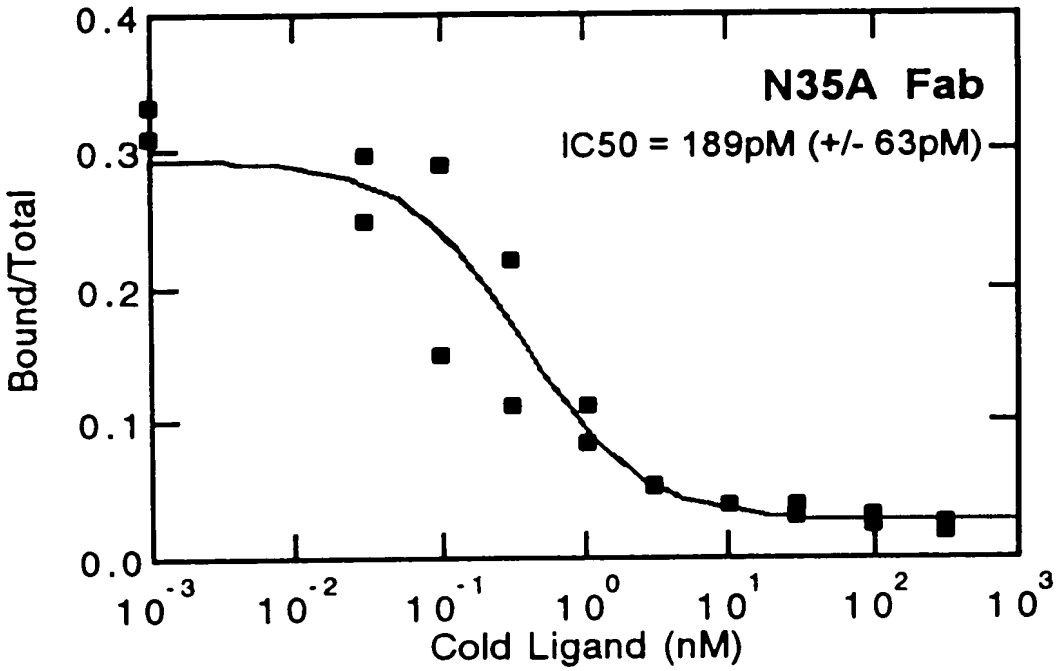


FIG. 43B

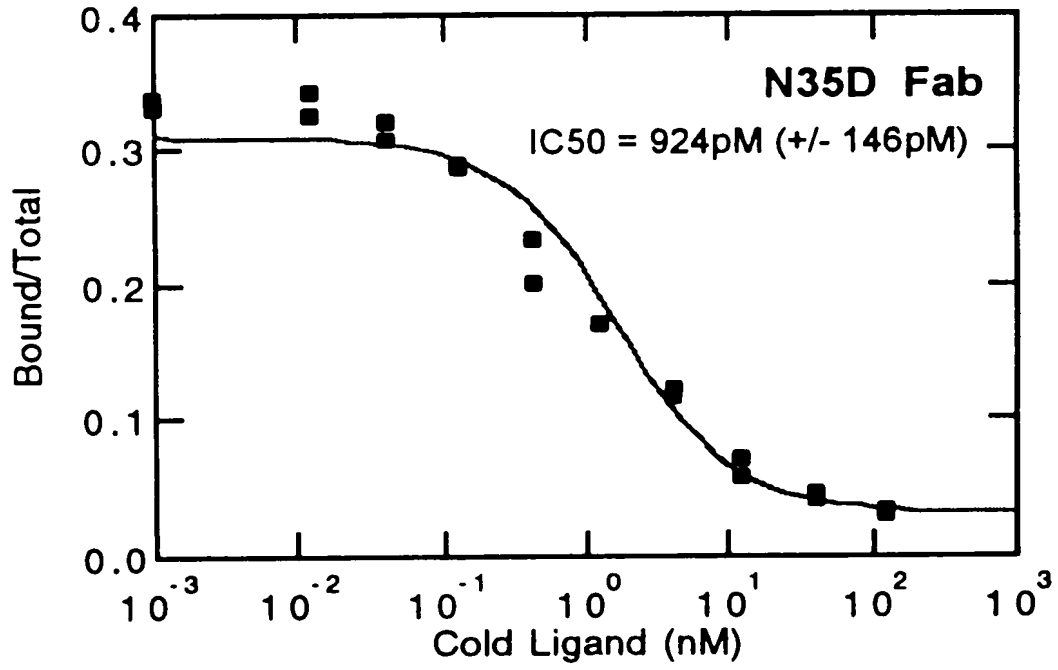


FIG. 43C

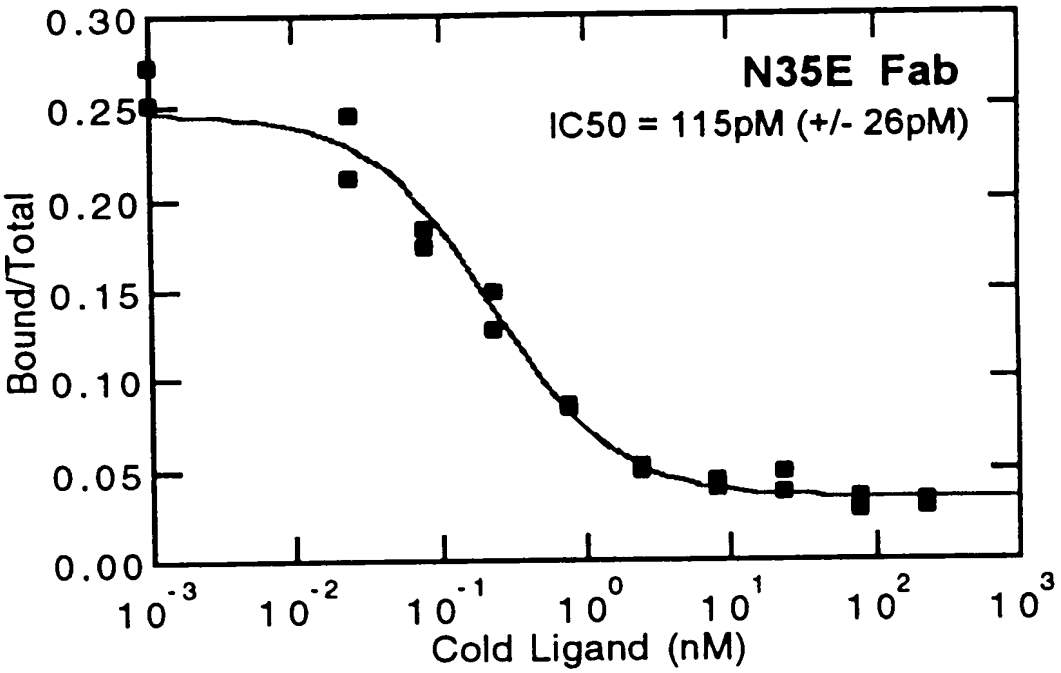


FIG. 43D

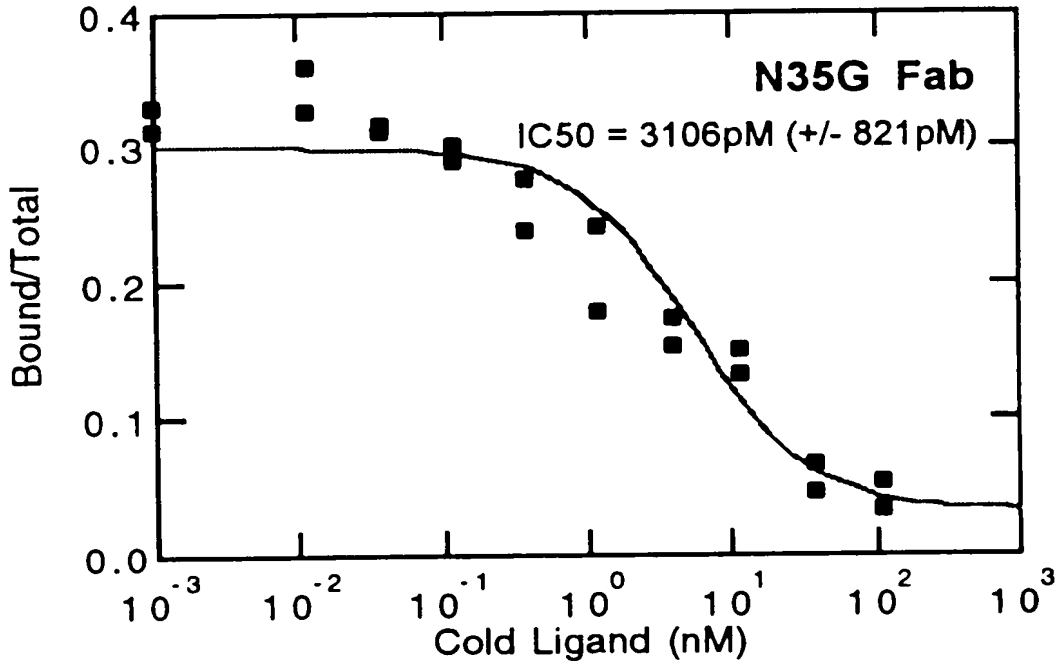
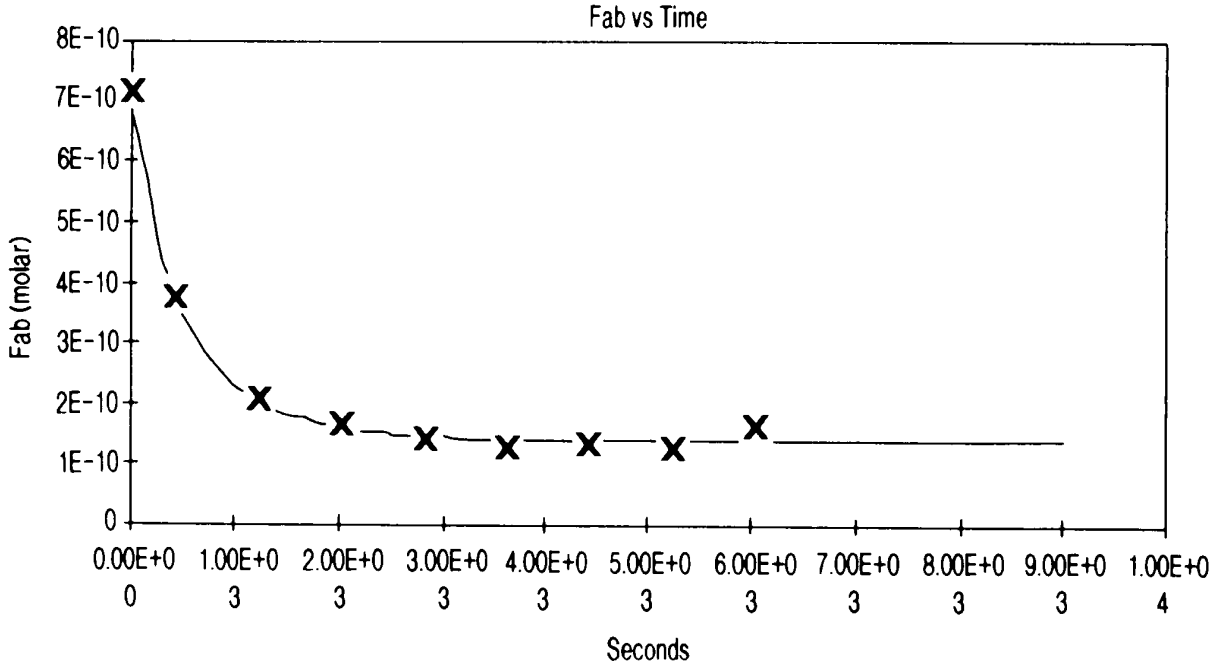


FIG. 43E



Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.F(ab')2.

SAMPLE	ka	kd	Kd
6G4V11N35A-Fab	ND	ND	114pM
6G4V11N35A-F(ab')$_2$	2.0×10^6	2.1×10^{-4}	109pM
6G4V11N35E-Fab	4.7×10^6	2.6×10^{-4}	54pM

FIG. 44

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M  K  K  N    I  A  F    L  L  A    S  M  F  V    F  S  I    A  T  N

 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
    CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
 -3 A  Y  A  D    I  Q  M    T  Q  S    P  S  S  L    S  A  S    V  G  D

121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGAGACGTAT
    TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACTCTGCATA
 18 R  V  T  I    T  C  R  S  S  Q    S  L  V  H    G  I  G    E  T  Y

181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
    AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
 38 L  H  W  Y    Q  Q  K    P  G  K    A  P  K  L    L  I  Y    K  V  S

241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
    TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
 58 N  R  F  S    G  V  P    S  R  F    S  G  S  G    S  G  T    D  F  T

301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT
    GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
 78 L  T  I  S    S  L  Q    P  E  D    F  A  T  Y    Y  C  S  Q  S  T

361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
    GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
 98 H  V  P  L  T    F  G    Q  G  T    K  V  E  I    K  R  T    V  A  A

421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
    GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
118 P  S  V  F    I  F  P    P  S  D    E  Q  L  K    S  G  T    A  S  V

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
    CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
138 V  C  L  L    N  N  F    Y  P  R    E  A  K  V    Q  W  K    V  D  N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
    CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCGTGG
158 A  L  Q  S    G  N  S    Q  E  S    V  T  E  Q    D  S  K    D  S  T

601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
    ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y  S  L  S    S  T  L    T  L  S    K  A  D  Y    E  K  H    K  V  Y

661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
    CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT
198 A  C  E  V    T  H  Q    G  L  S    S  P  V  T    K  S  F    N  R  G
                                                                  (SEQ ID NO.65)
721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
    CTCACAATTC GACTAGGAGA TGCGGCCTGC GTAGCACCGG GATCATGCGT TGATCAGCAT
218 E  C  O (SEQ ID NO.62)
```

FIG. 45

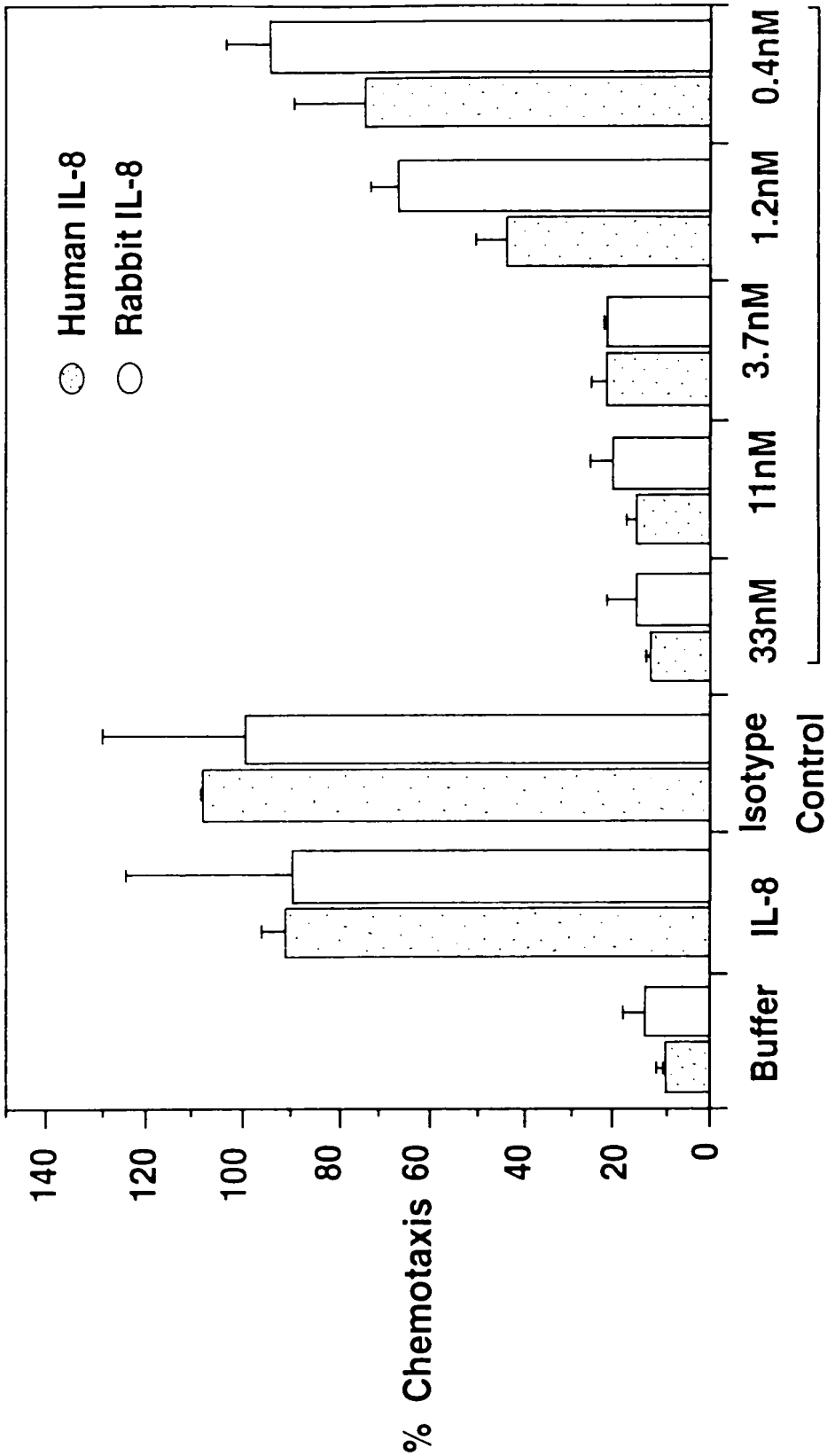


FIG. 46

N35AH1upr

5'-CTAGTGCAGTCTGGCGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCCTGTGCAGCTTCTGGCTACTCCTTC-3'
(SEQ ID NO.66)

N35AH1lwr

5'-TCGAGAAGGAGTAGCCAGAAGCTGCACAGGACAAACGGAGTGAGCCCCCTGGCTGCACCAGGCCACCGCCAGACTGCACT
AG-3'
(SEQ ID NO.67)

Bold indicates nucleotide change destroying PvuII site.

FIG. 47

```
> length: 8120 (circular)
>This has the pSVI backbone with the pRK7 cloning linker (pSVI7) and the intron DHFR(ID)
>made from pSVI.WTSD.D by adding a linearization linker(LL) into the Hpal site

         cac8I
        aluI
       sstI
       sacI                             sau3AI  aluI
       hgiJII                           mboI/ndeII[dam-]                                    scrFI
       hgiAI/aspHI                      dpnI[dam+]                                          mvaI
       ecl136II                        pvuI/bspCI                                           ecoRII
       bsp1286                     pleI dpnII[dam-]                                         dsaV
       bsiHKAI                     hinfI  taqI[dam-]                                        bstNI
       bmyI                    rmaI    mcrI    pvuII                                        apyI[dcm+]
       banII                   maeI    bsiEI   nspBII                                      bsaJI
     taqI                      bfaI   taqI[dam-]                                       bsmFI   nlaIV     cac8I
  1 TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGATC GACAGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA
    AAGCTCGAGC GGGCTGTAAC TAATAACTGA TCTCAGCTAG CTGTCGACAC CTTACACACA GTCAATCCCA CACCTTTCAG GGGTCCGAGG GGTCGTCCGT

                 sfaNI                                        scrFI                          sfaNI
               ppu10I                scrFI         mvaI                                    ppu10I
               nsiI/avaIII           mvaI               ecoRII                             nsiI/avaIII
              nlaIII                 ecoRII        dsaV                              nlaIII
             sphI                    dsaV          bstNI                                  sphI
             nspI                    bstNI              apyI[dcm+]                             nspI
             nspHI                   apyI[dcm+]        bsaJI                                   nspHI
             cac8I                  sexAI          bsmFI   nlaIV     cac8I                     cac8I
101 GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA
    CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTTGGTC CACACCTTTC AGGGGTCCGA GGGGTCGTCC GTCTTCATAC GTTTCGTACG TAGAGTTAAT

                                                                                        nlaIII
                                                                                       styI
                                                                                       ncoI
                 aciI                     aciI                                     bslI dsaI
               bsmFI           aciI   fokI              aciI bsrI  aciI            aciI bsaJI
201 GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT
    CAGTCGTTGG TATCAGGGCG GGGATTGAGG CGGGTAGGGC GGGGATTGAG GCGGGTCAAG GCGGGTAAGA GGCGGGGTAC CGACTGATTA AAAAAAATAA
```

FIG. 48A

```
                                                                                rmaI
                                                                                maeI
                    fnu4HI                                                     styI                              haeIII/palI
                    bsoFI                                                      bsaJI                   aluI     mcrI
                    bglI                                                       blnI                  rmaI       eagI/xmaIII/eclXI
                   sfiI                                                        avrII[dam-]           maeI       eaeI
                   haeIII/palI                                               haeIII/palI             bfaI       cfrI
                 mnlI   mnlI      ddeI                          mnlI        stuI                    nheI        bsiEI
            haeIII/palI bsaJI  mnlI   aluI                  mnlI            haeI                    cac8I      mspI
          mnlI bsaJI aciI   haeIII/palI                     bseRI          mnlI bfaI               aluI        hpaII
301 TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTA GCTTATCCGG
    ATACGTCTCC GGCTCCGGCG GAGCCGGAGA CTCGATAAGG TCTTCATCAC TCCTCCGAAA AAACCTCCGG ATCCGAAAAC GTTTTTCGAT CGAATAGGCC

                              tfiI
    scrFI                     hinfI
    nciI                   aciI                                                                     fnu4HI
    mspI                  thaI                                                                      bsoFI
    hpaII                 fnuDII/mvnI                        aciI                                   bbvI
    dsaV                  bstUI                    maeII  rsaI                                    nspBII
    cauII                 bsh1236I              maeIII    csp6I  scfI            mnlI             aciI       nlaIII
401 CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTGACGTAA GTACCGCCTA TAGAGCGATA AGAGGATTTT ATCCCCGCTG CCATCATGGT
    GGCCCTTGCC ACGTAACCTT GCGCCTAAGG GGCACGGTTC TCACTGCATT CATGGCGGAT ATCTCGCTAT TCTCCTAAAA TAGGGGCGAC GGTAGTACCA
                                                  ^splice donor                                       DHFR ATG^

                                                                               haeIII/palI
                                                                              haeI
                                                                            scrFI
                                                                            mvaI     bsrBI
                                                                            ecoRII
                                                                            dsaV
                                     pflMI                                  bstNI    aciI                   rsaI
                                     bslI                        bsmAI      apyI[dcm+]          xmnI        csp6I
    taqI           sfaNI         bsmFI                           bsaI      bsaJI  mnlI   ddeI   asp700     scaI
501 TCGACCATTG AACTGCATCG TCGCCGTGTC CCAAAATATG GGGATTGGCA AGAACGGAGA CCTACCCTGG CCTCCGCTCA GGAACGAGTT CAAGTACTTC
    AGCTGGTAAC TTGACGTAGC AGCGGCACAG GGTTTTATAC CCCTAACCGT TCTTGCCTCT GGATGGGACC GGAGGCGAGT CCTTGCTCAA GTTCATGAAG
```

FIG. 48B

```
                                                              scrFI
                                                              mvaI
                                                              ecoRII
        eco57I                                                dsaV
       mboII                      tfiI                        bstNI                 tfiI       tru9I
      earI/ksp632I                hinfI   hphI                apyI[dcm+]            hinfI      mseI
     mnlI                        alwNI[dcm-]                  sexAI           ddeI mboII taqI  ahaIII/draI
601 CAAAGAATGA CCACAACCTC TTCAGTGGAA GGTAAACAGA ATCTGGTGAT TATGGGTAGG AAAACCTGGT TCTCCATTCC TGAGAAGAAT CGACCTTTAA
    GTTTCTTACT GGTGTTGGAG AAGTCACCTT CCATTTGTCT TAGACCACTA ATACCCATCC TTTTGGACCA AGAGGTAAGG ACTCTTCTTA GCTGGAAATT

                                                    sstI
                                                    sacI
                                                    hgiJII
                                                    hgiAI/aspHI
                                                    ecl136II
                                                    bsp1286
                                                    bsiHKAI
                                                    bmyI
      tru9I                                      mnlI aluI                                   tru9I
      mseI         ddeI                        bssSI  banII                                  aflII/bfrI
     aseI/asnI/vspI                          bslI    bseRI           bstXI       fokI  sfaNI mseI
701 AGGACAGAAT TAATATAGTT CTCAGTAGAG AACTCAAAGA ACCACCACGA GGAGCTCATT TTCTTGCCAA AAGTTTGGAT GATGCCTTAA GACTTATTGA
    TCCTGTCTTA ATTATATCAA GAGTCATCTC TTGAGTTTCT TGGTGGTGCT CCTCGAGTAA AAGAACGGTT TTCAAACCTA CTACGGAATT CTGAATAACT

                                                                                      haeIII/palI
                                                                                     haeI
                                                            scrFI        scrFI
                                                            mvaI              mvaI
                                                            ecoRII       ecoRII
     mspI                                                   dsaV   tfiI  dsaV
     hpaII                                                  bstNI   nlaIII    bstNI    ddeI pleI
    bsaWI              accI nlaIII          mnlI            apyI[dcm+] hinfI apyI[dcm+]    hinfI
801 ACAACCGGAA TTGGCAAGTA AAGTAGACAT GGTTTGGATA GTCGGAGGCA GTTCTGTTTA CCAGGAAGCC ATGAATCAAC CAGGCCACCT TAGACTCTTT
    TGTTGGCCTT AACCGTTCAT TTCATCTGTA CCAAACCTAT CAGCCTCCGT CAAGACAAAT GGTCCTTCGG TACTTAGTTG GTCCGGTGGA ATCTGAGAAA
```

FIG. 48C

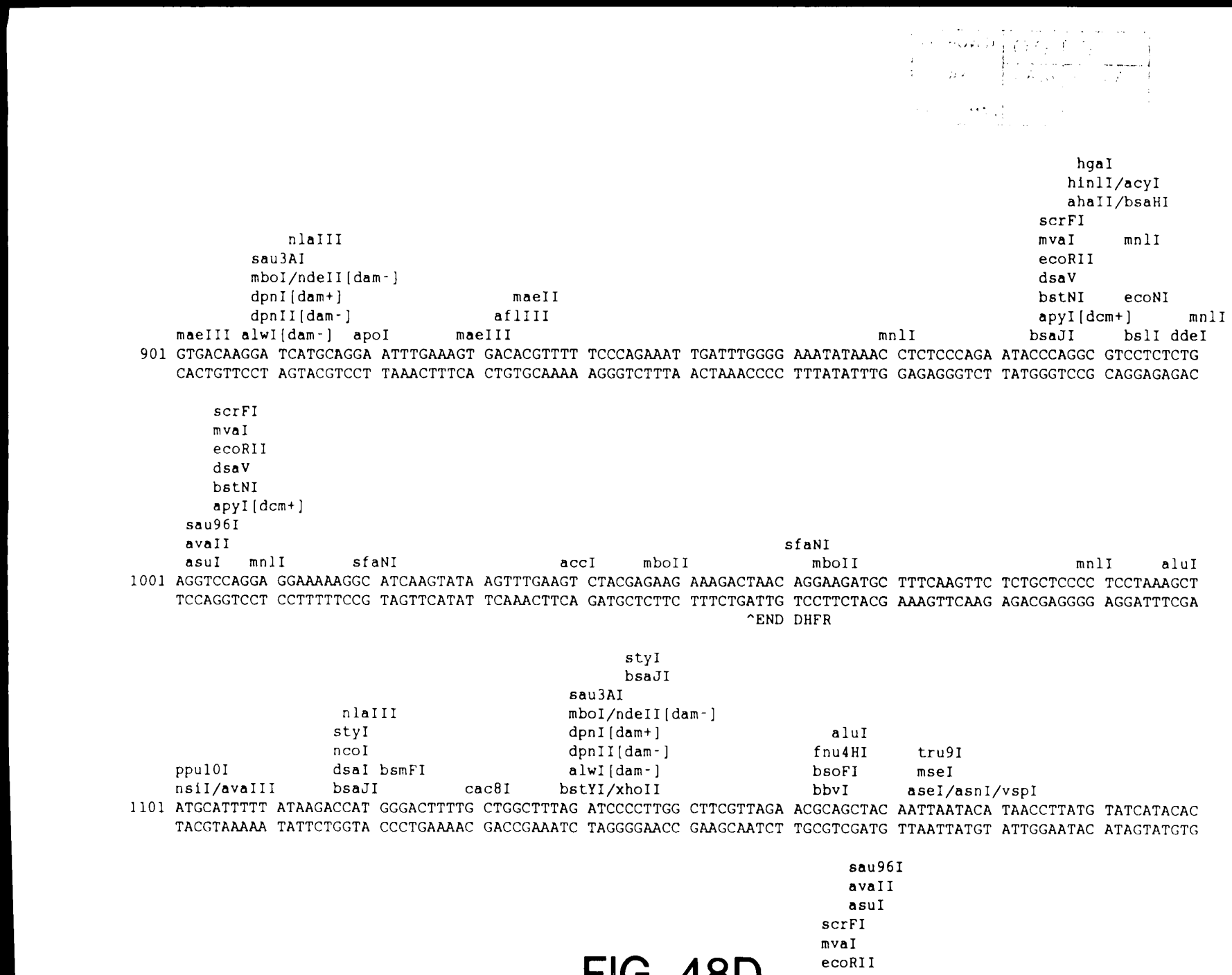


FIG. 48D

```
                                                                                    dsaV                              ecoRI
                                                                                    bstNI                             taqI    apoI
                                                                                    apyI[dcm+]        mnlI           claI/bsp106
        maeIII                                                            bslI      bsaJI             bsaJI          bspDI[dam-]
        hphI    scfI          fokI
1201 ATACGATTTA GGTGACACTA TAGATAACAT CCACTTTGCC TTTCTCTCCA CAGGTGTCCA CTCCCAGGTC CAACTGCACC TCGGTTCTAT CGATTGAATT
     TATGCTAAAT CCACTGTGAT ATCTATTGTA GGTGAAACGG AAAGAGAGGT GTCCACAGGT GAGGGTCCAG GTTGACGTGG AGCCAAGATA GCTAACTTAA
                                                                      seq from pRK6G425VH: Cla-AvrII^

                                                                                                         scrFI
                                                                                                         mvaI   fnu4HI
                                                                                                         ecoRII
                                                                                                         dsaV
                                                                                                         bstNI  bsoFI
      nlaIII                                                                                             apyI[dcm+]
      styI                                                                      rmaI                 haeI       bbvI
      pflMI                                                                     maeI              aciI haeIII/palI
      ncoI                                  rmaI              rsaI              bfaI
      dsaI                                  maeI        bpmI/gsuI[dcm-]      aluI
      bslI fokI                             bfaI        bsrI   csp6I
      bsaJI        nlaIII   fokI
1301 CCACCATGGG ATGGTCATGT ATCATCCTTT TTCTAGTAGC AACTGCAACT GGAGTACATT CAGAAGTTCA GCTAGTGCAG TCTGGCGGTG GCCTGGTGCA
     GGTGGTACCC TACCAGTACA TAGTAGGAAA AAGATCATCG TTGACGTTGA CCTCATGTAA GTCTTCAAGT CGATCACGTC AGACCGCCAC CGGACCACGT
   1                                                                   E  V  Q   L  V  Q   S  G  G  G   L  V  Q

                                                                                              scrFI
                                                                                              nciI
                                                                                              mspI
                                                                                              hpaII
                                                                                              dsaV
                                                                                              cauII
                                                                                             xmaI/pspAI
                                                                                             smaI
                                                                                             scrFI
                                                                                             nciI
                                                                                             dsaV        scrFI
                                                                                             cauII       mvaI
      hgiJII                                                                                 bslI        ecoRII
      bsp1286                                                                                bsaJI       dsaV
      bmyI                                                                             avaI          bstNI
    scrFI                                                                                  bsaJI          bslI
    mvaI banII                                          pleI                                          apyI[dcm+]
    ecoRII                     aluI               hinfI               sau96I    sau96I              haeIII/palI
    dsaV                     alwNI[dcm-]         taqI                 avaII     nlaIV          haeIII/palI   sau96I
    bstNI                        fnu4HI              xhoI                  asuI             asuI bslI   eco0109I/draII
    bsaJI                        bsoFI               paeR7I               nlaIV           eco0109I/draII asuI
    apyI[dcm+]                   bbvI                avaI    maeIII     bsrI
1401 GCCAGGGGGC TCACTCCGTT TGTCCTGTGC AGCTTCTGGC TACTCCTTCT CGAGTCACTA TATGCACTGG GTCCGTCAGG CCCCGGGTAA GGGCCTGGAA
     CGGTCCCCCG AGTGAGGCAA ACAGGACACG TCGAAGACCG ATGAGGAAGA GCTCAGTGAT ATACGTGACC CAGGCAGTCC GGGGCCCATT CCCGGACCTT
  14  P  G  G   S  L  R  L   S  C  A   A  S  G   Y  S  F  S   S  H  Y   M  H  W   V  R  Q  A   P  G  K   G  L  E
```

FIG. 48E

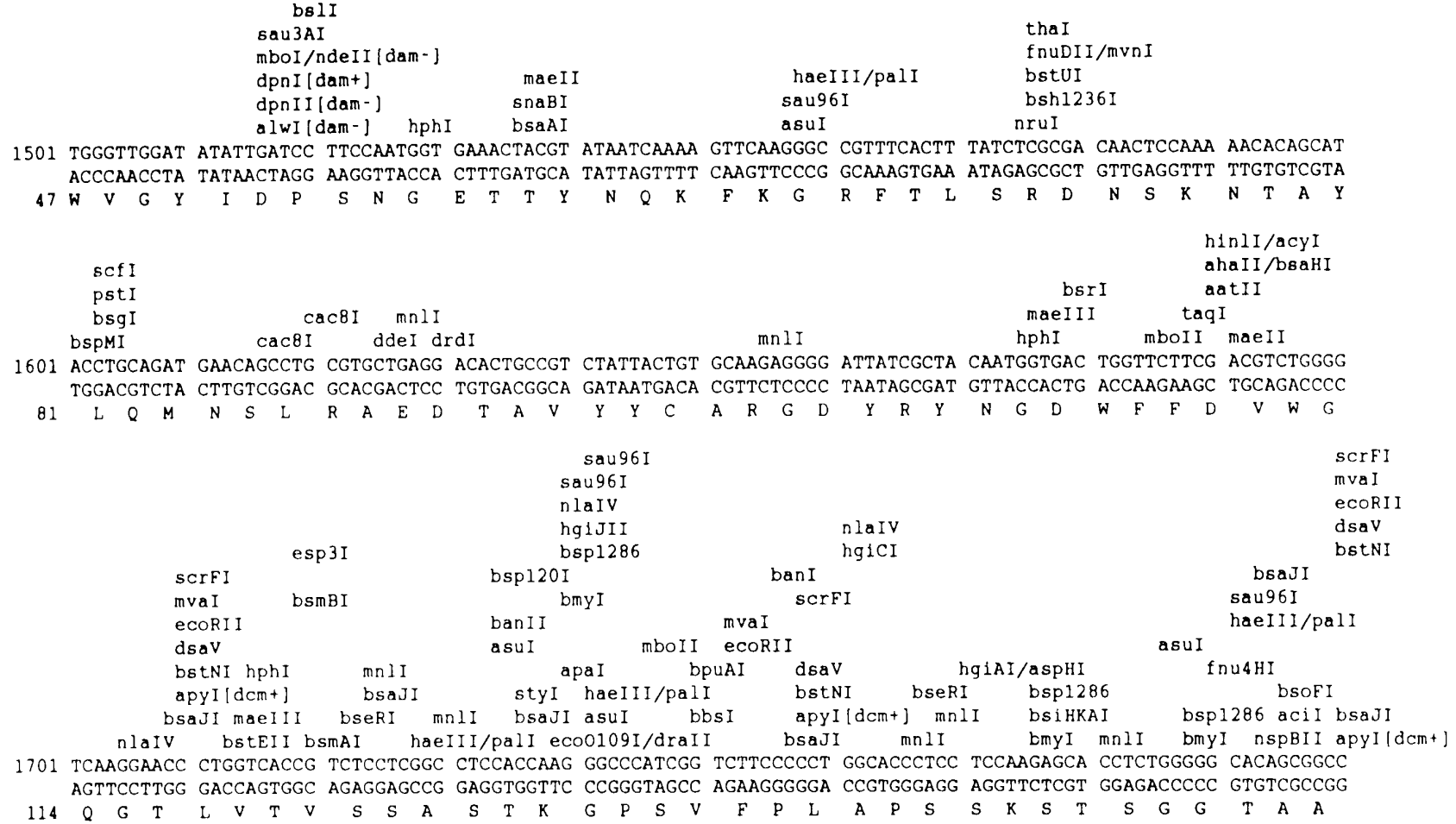


FIG. 48F

```
             scrFI
             mvaI                                                  hinPI
             ecoRII                                         nlaIV              hgiAI/aspHI
             ecoNI                                                narI               bsp1286
             dsaV                   maeIII                  kasI               bsiHKAI
             bstNI                       hphI                     hinlI/acyI         bmyI         mspI
             bslI                      mspI                       hgiCI            cac8I          hpaII
             apyI[dcm+]                hpaII                      haeII         fnu4HI           scrFI
         fnu4HI                       cfr10I/bsrFI                banI          bsoFI            nciI
         bsoFI                        bsaWI                       ahaII/bsaHI   aciI apaLI/snoI  dsaV
         bbvI                   bslI  ageI  tth111I/aspI     ddeI hhaI/cfoI nspBII  alw44I/snoI  cauII      scfI
1801 CTGGGCTGCC TGGTCAAGGA CTACTTCCCC GAACCGGTGA CGGTGTCGTG GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG GCTGTCCTAC
     GACCCGACGG ACCAGTTCCT GATGAAGGGG CTTGGCCACT GCCACAGCAC CTTGAGTCCG CGGGACTGGT CGCCGCACGT GTGGAAGGGC CGACAGGATG
147  L  G  C  L   V  K  D   Y  F  P   E  P  V  T   V  S  W   N  S  G   A  L  T  S   G  V  H   T  F  P   A  V  L  Q


                                                        fnu4HI
                                                        bsoFI    nlaIV
         ddeI pleI            fnu4HI                 rmaI        hgiCI
        mnlI  hinfI           bsoFI          bsp1286 maeI        banI                            tfiI
        eco81I           mnlI bbvI     maeIII        bfaI  aluI bsp1286                          hinfI
        bsu36I/mstII/sauI  ddeI       hphI   bmyI mnlI  bbvI    bmyI                    maeII
1901 AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGACTGT GCCCTCTAGC AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA
     TCAGGAGTCC TGAGATGAGG GAGTCGTCGC ACCACTGACA CGGGAGATCG TCGAACCCGT GGGTCTGGAT GTAGACGTTG CACTTAGTGT TCGGGTCGTT
181    S  S  G   L  Y  S   L  S  S  V   V  T  V   P  S  S   S  L  G  T   Q  T  Y   I  C  N   V  N  H  K   P  S  N

                                                                                                 ahdI/eam1105I
                                                                                                sau96I
                                                                                                avaII
                                                                                        scrFI
                                                                                        mvaI    asuI
                                                                                        ecoRII
                            hgiJII                                                      dsaV
       styI                 bsp1286                        nlaIII                       bstNI  nlaIV       mboII
       bsaJI                bmyI                         nspI         bsp1286           bsaJI  bsmFI      bpuAI
     mslI                   banII        maeIII          nspHI        bmyI alwNI[dcm-]  apyI[dcm+]        bbsI mnlI
2001 CACCAAGGTG GACAAGAAAG TTGAGCCCAA ATCTTGTGAC AAAACTCACA CATGCCCACC GTGCCCAGCA CCTGAACTCC TGGGGGGACC GTCAGTCTTC
     GTGGTTCCAC CTGTTCTTTC AACTCGGGTT TAGAACACTG TTTTGAGTGT GTACGGGTGG CACGGGTCGT GGACTTGAGG ACCCCCCTGG CAGTCAGAAG
214   T  K  V   D  K  K  V   E  P  K   S  C  D   K  T  H  T   C  P  P   C  P  A   P  E  L  L   G  G  P   S  V  F
```

FIG. 48G

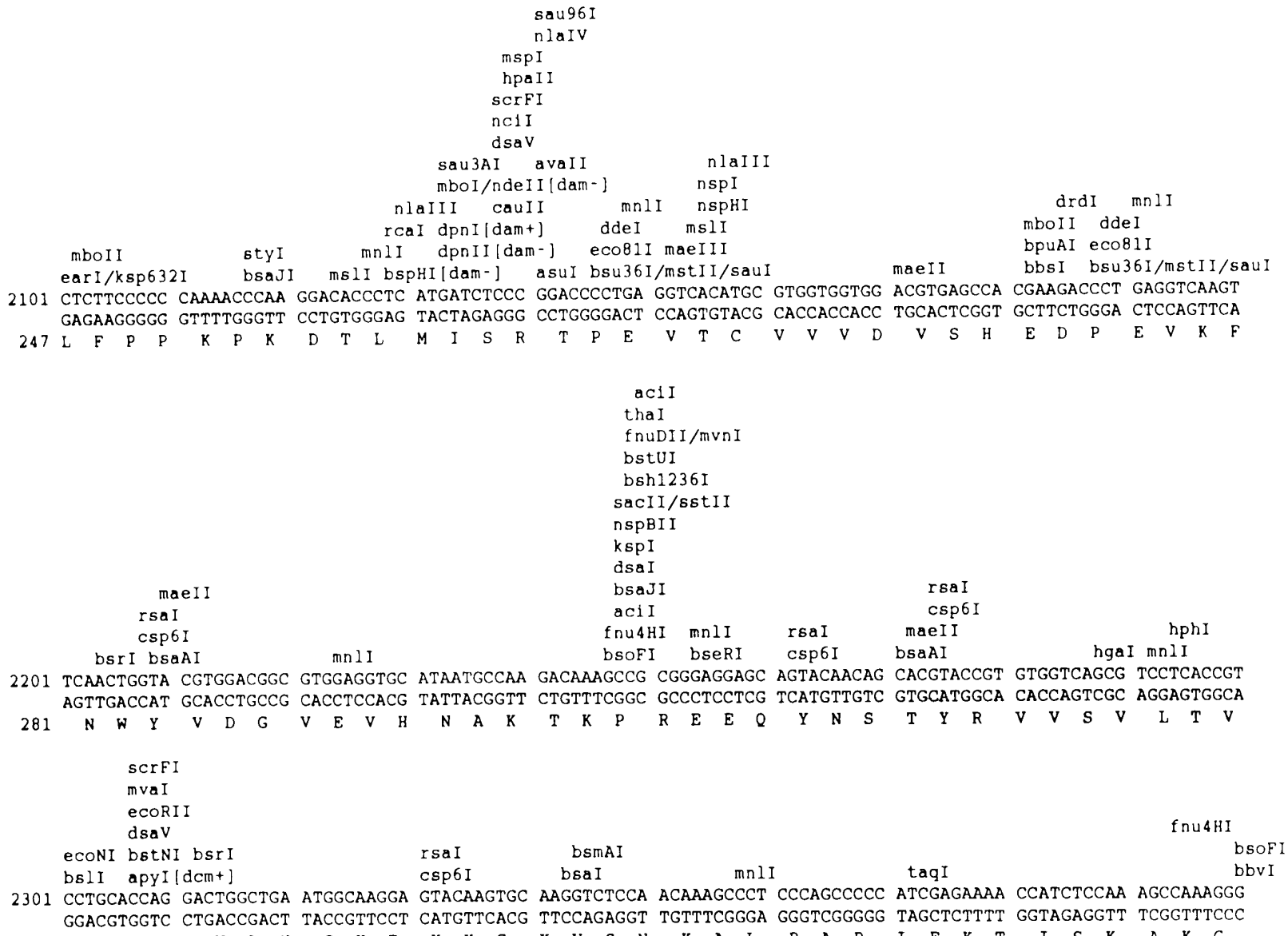


FIG. 48H

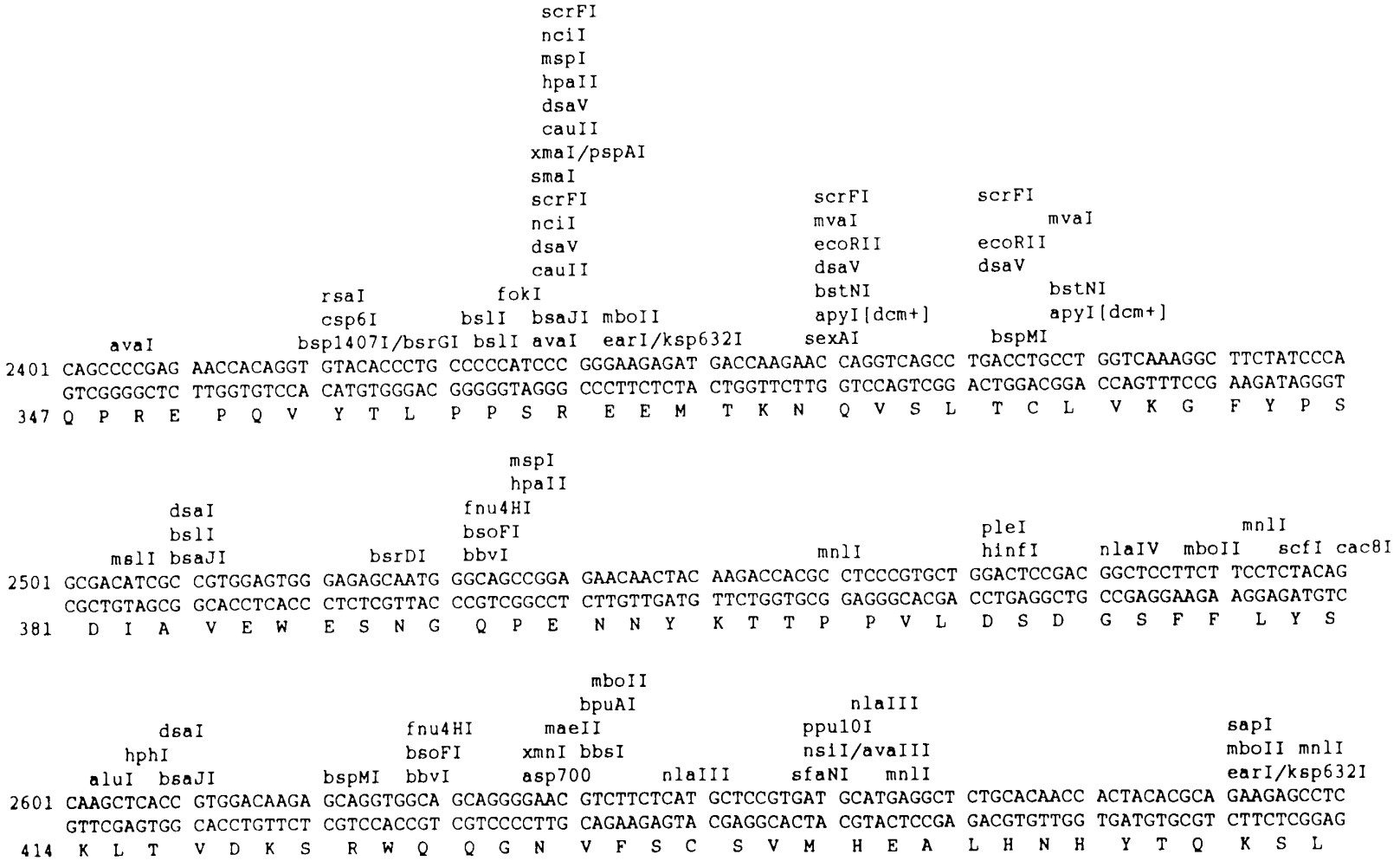


FIG. 48I

```
                                                                              sau96I
                                                                    aciI      haeIII/palI
          scrFI                              taqI                   fnu4HI    asuI
          nciI                            pleI                      bsoFI nlaIII
          mspI                         rmaI salI     scfI          sfiI   styI
          hpaII                        maeI hincII/hindII          eaeI   ncoI                   aluI
          dsaV                    sau96I  hinfI      pstI          cfrI   dsaI                 fnu4HI
      bsmAI                       haeIII/palI        bsgI     aluI haeIII/palI                 bsoFI
   bslI   cauII                   asuI bfaI accI bspMI      hindIII bglI bsaJI                 bbvI           maeIII
2701 TCCCTGTCTC CGGGTAAATG AGTGCGACGG CCCTAGAGTC GACCTGCAGA AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA
     AGGGACAGAG GCCCATTTAC TCACGCTGCC GGGATCTCAG CTGGACGTCT TCGAACCGGC GGTACCGGGT TGAACAAATA ACGTCGAATA TTACCAATGT
 447 S  L  S  P   G  K  O  (SEQ ID NO.71)

                                                                   rmaI
                                                                   maeI
             sfaNI  apoI                                      bsmI bfaI                                        nlaIII alwI[dam-]
2801 AATAAAGCAA TAGCATCACA AATTTCACAA ATAAAGCATT TTTTTCACTG CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG
     TTATTTCGTT ATCGTAGTGT TTAAAGTGTT TATTTCGTAA AAAAAGTGAC GTAAGATCAA CACCAAACAG GTTTGAGTAG TTACATAGAA TAGTACAGAC

        sau3AI
        mboI/ndeII[dam-]
        dpnI[dam+]
        dpnII[dam-]
       pvuI/bspCI
       mcrI
       bsiEI                                                                          rsaI
      taqI[dam-]  tru9I                                                               csp6I
     claI/bsp106[dam-]       fnu4HI     haeI                                         nlaIV
     bspDI[dam-]  mseI       bsoFI styI                                              kpnI
    sau3AI     xmnI          bbvI  ncoI                                              hgiCI
    mboI/ndeII[dam-]        hinPI  dsaI haeIII/palI                                  banI
    dpnI[dam+] asp700       hhaI/cfoI nlaIII                                         asp718     mnlI
    dpnII[dam-]  aseI/asnI/vspI    bsaJI          mnlI      mnlI                     acc65I   ddeI  aciI
2901 GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA AATAACCTCT GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA ACCATCTGTG
     CTAGCTAGCC CTTAATTAAG CCGCGTCGTG GTACCGGACT TTATTGGAGA CTTTCTCCTT GAACCAATCC ATGGAAGACT CCGCCTTTCT TGGTAGACAC
```

FIG. 48J

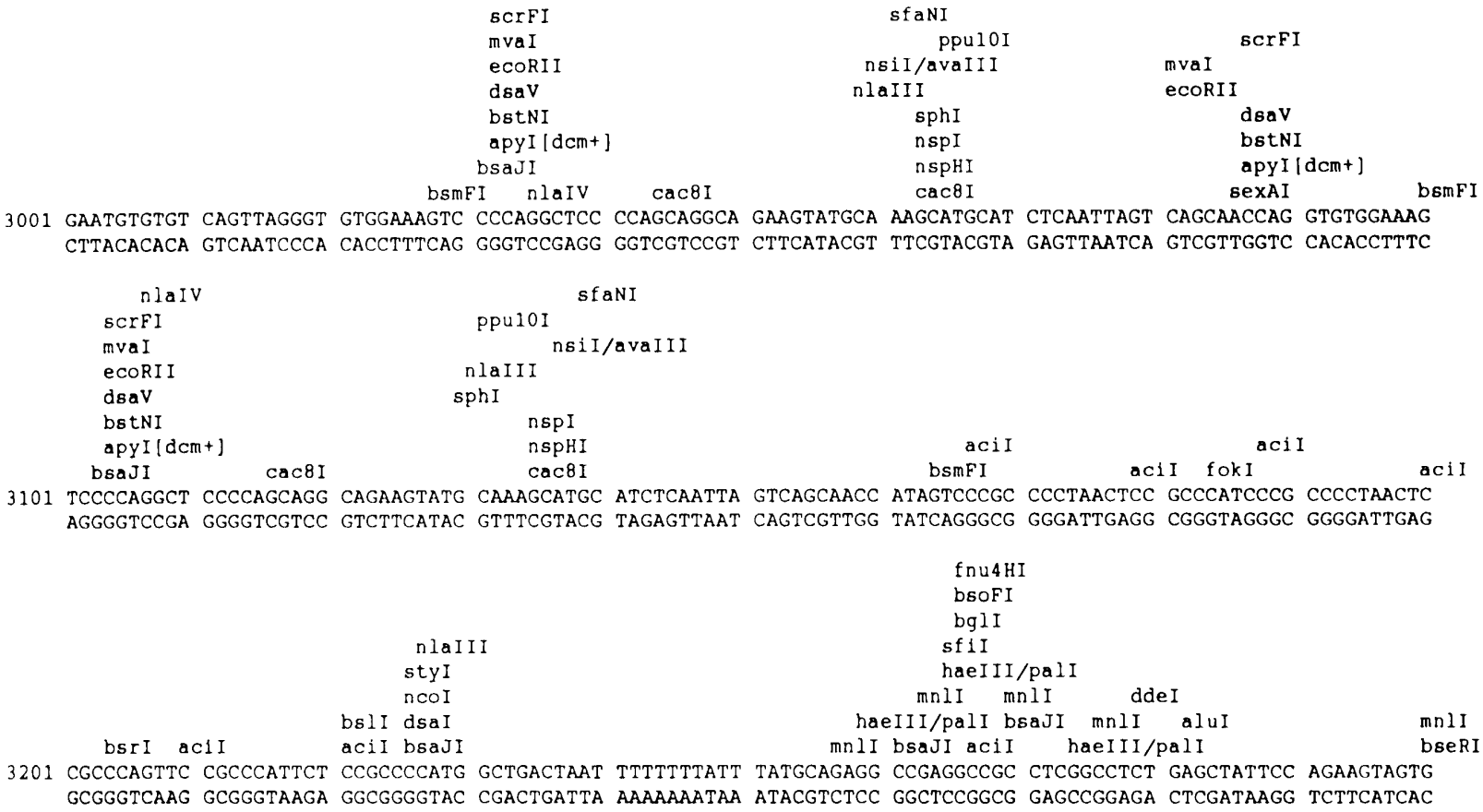


FIG. 48K

```
                                                   scrFI
                                                   nciI
                                                   mspI
                 rmaI                              hpaII
                 maeI                              dsaV
                styI                             haeIII/palI
                bsaJI                alu I       mcrI                                  tfiI
                blnI               rmaI          eagI/xmaIII/eclXI                       hinfI
                avrII[dam-]        maeI          eaeI                                  aciI
              haeIII/palI          bfaI          cfrI                                 thaI
             stuI                  nheI          bsiEI                                fnuDII/mvnI
             haeI                  cac8I        mspI cauII                            bstUI            pleI
   mnlI      mnlI bfaI            aluI          hpaII                                 bsh1236I         hinfI
3301 AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTA GCTTATCCGG CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTCAGGTAA
     TCCTCCGAAA AAACCTCCGG ATCCGAAAAC GTTTTTCGAT CGAATAGGCC GGCCCTTGCC ACGTAACCTT GCGCCTAAGG GGCACGGTTC TCAGTCCATT
                ^seq from pSVI6B5-6G4VL: AvrII - HindIII frag                       U1 matched splice donar^

                                                                                        sau3AI
                                                                                        mboI/ndeII[dam-]
                                                                                        dpnI[dam+]
                                                                                        dpnII[dam-]
                                                                                        alwI[dam-]
                                                                                      taqI[dam-]
                                                                                     claI/bsp106[dam-]
                                                   fnu4HI                            bspDI[dam-]
                                                   bsoFI                            sau3AI
                                    bstXI          aciI                             mboI/ndeII[dam-]
     aciI             scfI  sau96I    styI        thaI                              dpnI[dam+]
   rsaI         pleI        haeIII/palI           fnuDII/mvnI tru9I                 dpnII[dam-]
   csp6I  scfI  hinfI       asuI      bsaJI       bstUI      mseI                   alwI[dam-]                fokI
                                                  bsh1236I   aseI/asnI/vspI
3401 GTACCGCCTA TAGAGTCTAT AGGCCCACCC CCTTGGCTTC GTTAGAACGC GGCTACAATT AATACATAAC CTTTTGGATC GATCCTACTG ACACTGACAT
     CATGGCGGAT ATCTCAGATA TCCGGGTGGG GGAACCGAAG CAATCTTGCG CCGATGTTAA TTATGTATTG GAAAACCTAG CTAGGATGAC TGTGACTGTA
                                      ^sp6 promoter                           ^removed ATG
                                                                                        ^U2 match
                                                                                   lariat consensus^
                                                                          IgG vH natural lariat restored^
```

FIG. 48L

```
                                   sau96I
                                   avaII
                                   asuI                                         rmaI
                                 scrFI                                    maeI                                 nlaIII
                                 mvaI                                           bfaI                                styI
                                 ecoRII            thaI   nheI                          claI/bsp106      pflMI
                                 dsaV              fnuDII/mvnI                        sfaNI              ncoI
                                 bstNI                    bstUI  cac8I                 fnu4HI         ecoRI        dsaI
                                 apyI[dcm+]      mnlI     bsh1236I  aluI               bsoFI taqI     apoI         bslI fokI
                           bslI  bsaJI           bsaJI   nruI   aluI                   bbvI bspDI[dam-]            bsaJI
3501 CCACTTTTTC TTTTTCTCCA CAGGTGTCCA CTCCCAGGTC CAACTGCACC TCGGTTCGCG AAGCTAGCTT GGGCTGCATC GATTGAATTC CACCATGGGA
     GGTGAAAAAG AAAAAGAGGT GTCCACAGGT GAGGGTCCAG GTTGACGTGG AGCCAAGCGC TTCGATCGAA CCCGACGTAG CTAACTTAAG GTGGTACCCT
                                                     ^cloning linker

                                                                                          aluI
                                                                                         sstI
                                                                                         sacI
                                                                                         hgiJII
                                                                                         hgiAI/aspHI
                                                                                         ecl136II
                                                                                         bsp1286
                                                                                         bsiHKAI
                                                                                   bsmFI bmyI
                         rmaI                rsaI                               bsrI   avaI                 mnlI
                         maeI           bpmI/gsuI[dcm-]                                                   aciI
       nlaIII   fokI     bfaI           bsrI   csp6I       ecoRV           tth111I/aspI banII
3601 TGGTCATGTA TCATCCTTTT TCTAGTAGCA ACTGCAACTG GAGTACATTC AGATATCCAG ATGACCCAGT CCCCGAGCTC CCTGTCCGCC TCTGTGGGCG
     ACCAGTACAT AGTAGGAAAA AGATCATCGT TGACGTTGAC CTCATGTAAG TCTATAGGTC TACTGGGTCA GGGGCTCGAG GGACAGGCGG AGACACCCGC
1                                                             D  I  Q   M  T  Q  S   P  S  S   L  S  A   S  V  G  D

                      scfI                                                                          scrFI
                      pstI                                                                          mvaI
                      bsgI                      rsaI                                                ecoRII
         hphI        sse8387I             ddeI                     maeII                            dsaV
        maeIII      bspMI               aluI  csp6I                snaBI                            bstNI      aluI
      bstEII      hphI  bspMI          hindIII     nlaIII          bsaAI         bsrI               apyI[dcm+]
3701 ATAGGGTCAC CATCACCTGC AGGTCAAGTC AAAGCTTAGT ACATGGTATA GGTGCTACGT ATTTACACTG GTATCAACAG AAACCAGGAA AAGCTCCGAA
     TATCCCAGTG GTAGTGGACG TCCAGTTCAG TTTCGAATCA TGTACCATAT CCACGATGCA TAAATGTGAC CATAGTTGTC TTTGGTCCTT TTCGAGGCTT
18    R  V  T   I  T  C   R  S  S  Q   S  L  V   H  G  I   G  A  T  Y   L  H  W   Y  Q  Q   K  P  G  K   A  P  K
```

FIG. 48M

```
                                                                 mspI
                                                                 hpaII
                                                                 bslI
                                                                bsaWI
                                                               sau3AI
                                                               mboI/ndeII[dam-]
                                                               dpnI[dam+]
                                                               dpnII[dam-]
                                                               alwI[dam-]                          fnu4HI
                      tfiI                                    nlaIV                                bsoFI
                      hinfI      bsmFI                        bstYI/xhoII                          bbvI
                     taqI     bpmI/gsuI[dcm-]                 bamHI                               scfI
                    claI/bsp106  pleI                         alwI[dam-]   bsmFI                  pstI
                    bspDI[dam-]  hinfI                                                            bsgI
3801 ACTACTGATT TACAAAGTAT CCAATCGATT CTCTGGAGTC CCTTCTCGCT TCTCTGGATC CGGTTCTGGG ACGGATTTCA CTCTGACCAT CAGCAGTCTG
     TGATGACTAA ATGTTTCATA GGTTAGCTAA GAGACCTCAG GGAAGAGCGA AGAGACCTAG GCCAAGACCC TGCCTAAAGT GAGACTGGTA GTCGTCAGAC
  51  L  L  I   Y  K  V  S   N  R  F   S  G  V   P  S  R  F   S  G  S   G  S  G   T  D  F  T   L  T  I   S  S  L

                                                                         rsaI
                                                                         csp6I
                                                                        nlaIV
                                                                        kpnI styI
                                                     bsrBI              hgiCI              sau3AI
        mboII                            rsaI        aciI               banI bsaJI         mboI/ndeII[dam-] fnu4HI
        bpuAI                            csp6I     bsmFI                asp718             dpnI[dam+]       bsoFI
        bbsI                            scaI    nlaIII        maeII     acc65I             dpnII[dam-]      bbvI
3901 CAGCCAGAAG ACTTCGCAAC TTATTACTGT TCACAGAGTA CTCATGTCCC GCTCACGTTT GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGCTG
     GTCGGTCTTC TGAAGCGTTG AATAATGACA AGTGTCTCAT GAGTACAGGG CGAGTGCAAA CCTGTCCCAT GGTTCCACCT CTAGTTTGCT TGACACCGAC
  84 Q  P  E  D   F  A  T   Y  Y  C   S  Q  S  T   H  V  P   L  T  F   G  Q  G  T   K  V  E   I  K  R   T  V  A  A

                                                                                                     haeIII/palI
          mboII                                                                                      haeI
         bpuAI                                            xmnI                       xmnI           mnlI
         bbsI      mboII  aciI                            asp700            cac8I    asp700
4001 CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCTTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA
     GTGGTAGACA GAAGTAGAAG GGCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGAAGAC AACACACGGA CGACTTATTG AAGATAGGGT CTCTCCGGTT
 118  P  S  V   F  I  F   P  P  S  D   E  Q  L   K  S  G   T  A  S  V   V  C  L   L  N  N   F  Y  P  R   E  A  K
```

FIG. 48N

```
                                                 scrFI
                                                 mvaI
                                                 ecoRII
                                                 dsaV
                                                 bstNI
                                                 apyI[dcm+]                                            fnu4HI
      rsaI                    mnlI                                                            ddeI bsoFI
      csp6I                   bslI       maeIII  bsaJI      maeIII                     scfI   mnlI  bbvI
4101 AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTCACAGA GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC
     TCATGTCACC TTCCACCTAT TGCGGGAGGT TAGCCCATTG AGGGTCCTCT CACAGTGTCT CGTCCTGTCG TTCCTGTCGT GGATGTCGGA GTCGTCGTGG
151  V  Q  W   K  V  D  N   A  L  Q   S  G  N   S  Q  E  S   V  T  E   Q  D  S   K  D  S  T   Y  S  L   S  S  T

                                                                            sstI
                                                                            sacI
                                                                            hgiJII
                                                                            hgiAI/aspHI
                                                                            ecl136II
                                                                            bsp1286
                                                                            bsiHKAI
                                                                            bmyI
                                                                          ddeI cac8I
                                                                       haeIII/palI
        ddeI                                                          sau96I aluI
       celII/espI                                                     asuI   banII
       blpI/bpu1102I                                    hphI          eco0109I/draII
     hgaI                                   accI   cac8I    maeIII    alwNI[dcm-]      maeIII    aluI
4201 CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA AGTCACCCAT CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG
     GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TGCGGACGCT TCAGTGGGTA GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCCC
184  L  T  L  S   K  A  D   Y  E  K   H  K  V  Y   A  C  E   V  T  H   Q  G  L  S   S  P  V   T  K  S   F  N  R  G

                             sau96I
                      aciI   haeIII/palI
                     fnu4HI  asuI
                     bsoFI nlaIII
                     sfiI  styI
                 aluI haeIII/palI                 aluI
               hindIII bglI ncoI                  fnu4HI
             tru9I  eaeI  dsaI                    bsoFI
             mseI   cfrI  bsaJI                   bbvI      maeIII              sfaNI  apoI
4301 GAGAGTGTTA AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA AATAAAGCAA TAGCATCACA AATTTCACAA ATAAAGCATT
     CTCTCACAAT TCGAACCGGC GGTACCGGGT TGAACAAATA ACGTCGAATA TTACCAATGT TTATTTCGTT ATCGTAGTGT TTAAAGTGTT TATTTCGTAA
218   E  C  O (SEQ ID NO.72)
```

FIG. 48O

```
                                                                 sau3AI
                                                                 mboI/ndeII[dam-]
                                                                 dpnI[dam+]
                                                                 dpnII[dam-]
                                                                pvuI/bspCI
                                                                mcrI
                                                                bsiEI
                                                               taqI[dam-]
                                                              claI/bsp106[dam-]
                                                              bspDI[dam-]  tru9I      fnu4HI    haeI
                                                             sau3AI        mseI       bsoFI styI
                                                             mboI/ndeII[dam-]         bbvI  ncoI
                 rmaI                                        dpnI[dam+] xmnI         hinPI  dsaI haeIII/palI
                 maeI                                        dpnII[dam-]  aseI/asnI/vspI    bsaJI
           bsmI  bfaI                                 nlaIII alwI[dam-]   asp700     hhaI/cfoI nlaIII
4401 TTTTTCACTG CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA
     AAAAAGTGAC GTAAGATCAA CACCAAACAG GTTTGAGTAG TTACATAGAA TAGTACAGAC CTAGCTAGCC CTTAATTAAG CCGCGTCGTG GTACCGGACT
                                                                              ^sv40

                            rsaI                                                                    scrFI
                             csp6I                                                                  mvaI
                            nlaIV                                                                   ecoRII
                            kpnI                                                                    dsaV
                            hgiCI                                                                   bstNI
                            banI                          aluI                                      apyI[dcm+]
                            asp718      mnlI             pvuII                                     bsaJI
       mnlI       mnlI      acc65I     ddeI  aciI        nspBII                                bsmFI   nlaIV
4501 AATAACCTCT GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA ACCAGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC
     TTATTGGAGA CTTTCTCCTT GAACCAATCC ATGGAAGACT CCGCCTTTCT TGGTCGACAC CTTACACACA GTCAATCCCA CACCTTTCAG GGGTCCGAGG

                          sfaNI                                      scrFI                           sfaNI
                        ppu10I                  scrFI        mvaI                                   ppu10I
                        nsiI/avaIII             mvaI                 ecoRII                         nsiI/avaIII
                       nlaIII                   ecoRII       dsaV                           nlaIII
                      sphI                      dsaV         bstNI                               sphI
                      nspI                      bstNI               apyI[dcm+]                          nspI
                      nspHI                     apyI[dcm+]         bsaJI                                nspHI
     cac8I            cac8I                    sexAI          bsmFI   nlaIV     cac8I                   cac8I
4601 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC
     GGTCGTCCGT CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTTGGTC CACACCTTTC AGGGGTCCGA GGGGTCGTCC GTCTTCATAC GTTTCGTACG
```

FIG. 48P

FIG. 48Q

```
                                                                                                sau3AI
                                                                                                mboI/ndeII[dam-]
                                                                                     sau96I     dpnI[dam+]
                                                               cac8I                 haeIII/palI
                                                               aluI                  asuI       dpnII[dam-]
                                    fnu4HI                    pvuII               mnlI aciI  pvuI/bspCI
                   tru9I            bsoFI                     nspBII            mboII cac8I  mcrI
       maeIII      mseI             bbvI     fokI           cac8I               earI/ksp632I bsiEI
5001 TGGCGTTACC CAACTTAATC GCCTTGCAGC ACATCCCCCC TTCGCCAGCT GGCGTAATAG CGAAGAGGCC CGCACCGATC GCCCTTCCCA ACAGTTGCGT
     ACCGCAATGG GTTGAATTAG CGGAACGTCG TGTAGGGGGG AAGCGGTCGA CCGCATTATC GCTTCTCCGG GCGTGGCTAG CGGGAAGGGT TGTCAACGCA

                 hinPI
                 hhaI/cfoI
                nlaIV
                narI
                kasI                                                                                  hinPI
                hinlI/acyI                                                                           thaI
                hgiCI                                                                                fnuDII/mvnI
                haeII      aciI                                                                      bstUI scfI
                banI     sfaNI                                                                       bsh1236I
                ahaII/bsaHI                                                                       rsaI hhaI/cfoI
     bglI                                            sfaNI    aciI           aciI    maeII        csp6I    bslI
5101 AGCCTGAATG GCGAATGGCG CCTGATGCGG TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TACGTCAAAG CAACCATAGT ACGCGCCCTG
     TCGGACTTAC CGCTTACCGC GGACTACGCC ATAAAAGAGG AATGCGTAGA CACGCCATAA AGTGTGGCGT ATGCAGTTTC GTTGGTATCA TGCGCGGGAC

                  aciI
                fnu4HI                 fnu4HI
                bsoFI                  bsoFI
               thaI                   hinPI                                   hinPI
               fnuDII/mvnI            hhaI/cfoI                               hhaI/cfoI
        hinPI     bstUI              thaI                                  rmaI
        hhaI/cfoI hinPI              fnuDII/mvnI                        hinPI  haeII
      fnu4HI      hhaI/cfoI          bstUI                              hhaI/cfoI    bsrBI
      bsoFI    tru9I aciI            bsh1236I      aciI                haeII maeI    aciI
      aciI     mseI bsh1236I      maeIII bbvI  maeIII        cac8I     bfaI  cac8I           mboII
5201 TAGCGGCGCA TTAAGCGCGG CGGGTGTGGT GGTTACGCGC AGCGTGACCG CTACACTTGC CAGCGCCCTA GCGCCCGCTC CTTTCGCTTT CTTCCCTTCC
     ATCGCCGCGT AATTCGCGCC GCCCACACCA CCAATGCGCG TCGCACTGGC GATGTGAACG GTCGCGGGAT CGCGGGCGAG GAAAGCGAAA GAAGGGAAGG
```

FIG. 48R

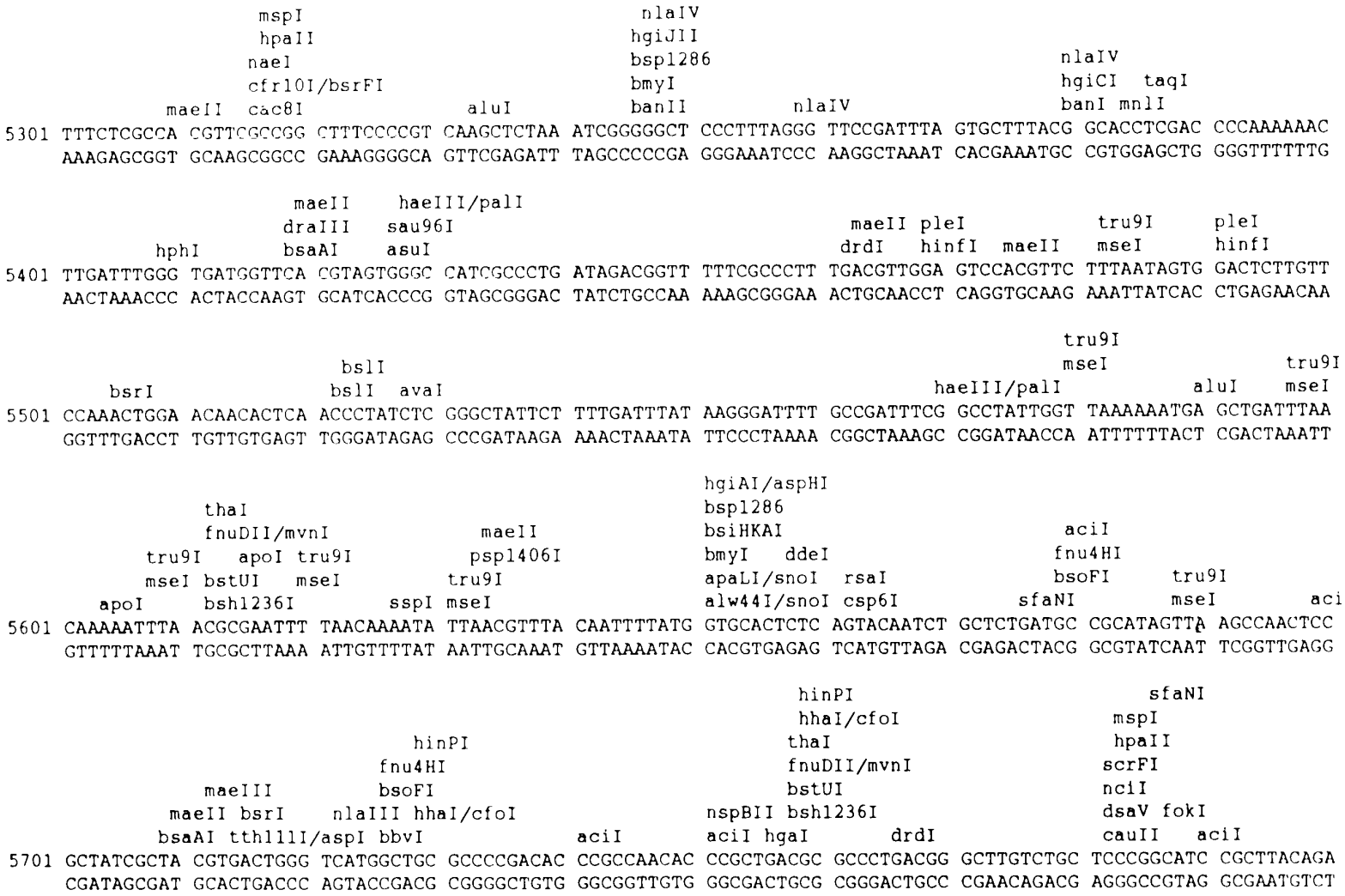


FIG. 48S

```
                                                                      thaI
                                                                      fnuDII/mvnI
                 scrFI                                                bstUI
                 nciI                                                 bsh1236I
                 mspI                                                hinPI
                 hpaII      nspI                                     hhaI/cfoI                             mnlI
                 dsaV       nspHI                                   thaI mnlI                            haeIII/palI
            esp3I        fnu4HI                                     fnuDII/mvnI          mboII         sau96I
            bsmBI        bsoFI                                      bstUI                bpuAI         asuI bssSI
       maeIII bsmAI      bbvI                                       bsh1236I             bbsI         eco0109I/draII
    aluI    bslI   cauII aluI nlaIII     mnlI      hphI      hphI
5801 CAAGCTGTGA CCGTCTCCGG GAGCTGCATG TGTCAGAGGT TTTCACCGTC ATCACCGAAA CGCGCGAGGC AGTATTCTTG AAGACGAAAG GGCCTCGTGA
     GTTCGACACT GGCAGAGGCC CTCGACGTAC ACAGTCTCCA AAAGTGGCAG TAGTGGCTTT GCGCGCTCCG TCATAAGAAC TTCTGCTTTC CCGGAGCACT

                                                                                         nlaIV
                                                                                       aciI
                                                                                      thaI
                                                                                      fnuDII/mvnI
                                                          hinlI/acyI                  bstUI
                            nlaIII                        ahaII/bsaHI                 bsh1236I
                      tru9I rcaI                          aatII                      hinPI
                      mseI  bspHI                    ddeI maeII                      hhaI/cfoI
5901 TACGCCTATT TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT
     ATGCGGATAA AAATATCCAA TTACAGTACT ATTATTACCA AAGAATCTGC AGTCCACCGT GAAAAGCCCC TTTACACGCG CCTTGGGGAT AAACAAATAA

                               rcaI
                               bspHI
                            bsrBI    bsmAI                                        mboII
                            aciI   nlaIII                           sspI          earI/ksp632I        mslI
6001 TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGAT AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTC
     AAAGATTTAT GTAAGTTTAT ACATAGGCGA GTACTCTGTT ATTGGGACTA TTTACGAAGT TATTATAACT TTTTCCTTCT CATACTCATA AGTTGTAAAG

                                                                                                          hgiAI/aspHI
                                                                                                          bsp1286
                                                                                               sau3AI     bsiHKAI
                                                                                               mboI/ndeII[dam-]
                                                                                               dpnI[dam+] bmyI
                           fnu4HI                                                              dpnII[dam-]
                           bsoFI                                                           eco57I         apaLI/snoI
                           aciI                                 hphI          hphI      sfaNI  mboII[dam-] alw44I/snoI
6101 CGTGTCGCCC TTATTCCCTT TTTTGCGGCA TTTTGCCTTC CTGTTTTTGC TCACCCAGAA ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG
     GCACAGCGGG AATAAGGGAA AAAACGCCGT AAAACGGAAG GACAAAAACG AGTGGGTCTT TGCGACCACT TTCATTTTCT ACGACTTCTA GTCAACCCAC
```

FIG. 48T

```
                           sau3AI    nspBII     sau3AI
                           mboI/ndeII[dam-]     mboI/ndeII[dam-]             maeII
                           dpnI[dam+]           dpnI[dam+]                  psp1406I          hgiAI/aspHI
                          bstYI/xhoII           dpnII[dam-]                xmnI              bsp1286   tru9I
                      bsrI dpnII[dam-]          alwI[dam-]                 asp700            bsiHKAI   mseI
                                                                          mboII              bmyI    ahaIII/draI
     bssSI    maeIII taqI    alwI[dam-]   aciI bstYI/xhoII
6201 CACGAGTGGG TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG AGTTTTCGCC CCGAAGAACG TTTTCCAATG ATGAGCACTT TTAAAGTTCT
     GTGCTCACCC AATGTAGCTT GACCTAGAGT TGTCGCCATT CTAGGAACTC TCAAAAGCGG GGCTTCTTGC AAAAGGTTAC TACTCGTGAA AATTTCAAGA

                                  scrFI
          aciI                    nciI
         thaI                     mspI
         fnuDII/mvnI              hpaII
         bstUI                    dsaV
         bsh1236I             hinlI/acyI                  aciI                               rsaI
        hinPI                 hgaI cauII             mcrI  fnu4HI                            csp6I    bsrI
        hhaI/cfoI             ahaII/bsaHI      bcgI  bsiEI bsoFI          ddeI              scaI   hphI  maeIII
6301 GCTATGTGGC GCGGTATTAT CCCGTGATGA CGCCGGGCAA GAGCAACTCG GTCGCCGCAT ACACTATTCT CAGAATGACT TGGTTGAGTA CTCACCAGTC
     CGATACACCG CGCCATAATA GGGCACTACT GCGGCCCGTT CTCGTTGAGC CAGCGGCGTA TGTGATAAGA GTCTTACTGA ACCAACTCAT GAGTGGTCAG

                                                                                                       sau3AI
                                                                                   haeIII/palI         mboI/ndeII[dam-]
                                                                                  eaeI                 dpnI[dam+]
                                                                                  cfrI                 dpnII[dam-]
                                                    fnu4HI                       fnu4HI               pvuI/bspCI
                                                    bsoFI                        bsoFI                mcrI
        sfaNI     fokI    nlaIII                    bbvI   mslI   nlaIII         aciI                 bsiEI
6401 ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC TGCCATAACC ATGAGTGATA ACACTGCGGC CAACTTACTT CTGACAACGA
     TGTCTTTTCG TAGAATGCCT ACCGTACTGT CATTCTCTTA ATACGTCACG ACGGTATTGG TACTCACTAT TGTGACGCCG GTTGAATGAA GACTGTTGCT

                                                   nlaIII
                                                 sau3AI maeIII                    mspI
                                                 mboI/ndeII[dam-]    sau3AI    nlaIV
       sau96I                                    dpnI[dam+]          mboI/ndeII[dam-] aluI
       avaII                                     dpnII[dam-]         dpnI[dam+]    hpaII
       asuI                                                          dpnII[dam-] bsaWI
     mnlI          aluI    aciI            nlaIII alwI[dam-]
6501 TCGGAGGACC GAAGGAGCTA ACCGCTTTTT TGCACAACAT GGGGGATCAT GTAACTCGCC TTGATCGTTG GGAACCGGAG CTGAATGAAG CCATACCAAA
     AGCCTCCTGG CTTCCTCGAT TGGCGAAAAA ACGTGTTGTA CCCCCTAGTA CATTGAGCGG AACTAGCAAC CCTTGGCCTC GACTTACTTC GGTATGGTTT
```

FIG. 48U

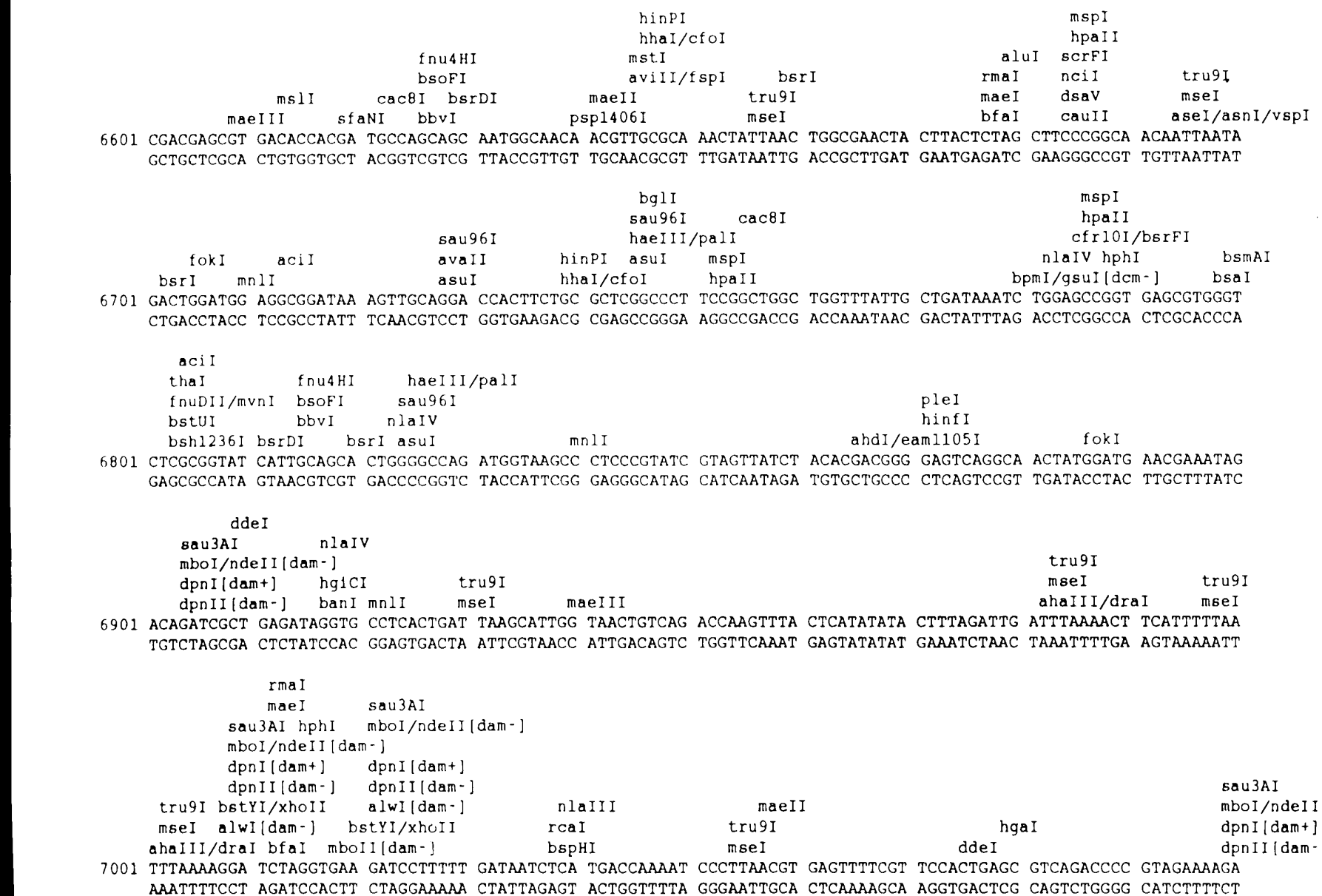


FIG. 48V

```
                   sau3AI
          mboII[dam-]
        sau3AI       mboI/ndeII[dam-] thaI
        mboI/ndeII[dam-]             fnuDII/mvnI
        dpnI[dam+]  dpnI[dam+]       bstUI         cac8I
        dpnII[dam-] dpnII[dam-]      bsh1236I   fnu4HI
       bstYI/xhoII  alwI[dam-]      hinPI       bsoFI                              aciI               mspI
       alwI[dam-]  bstYI/xhoII      hhaI/cfoI   bbvI                    aciI     nspBII             hpaII      aluI
7101 TCAAAGGATC TTCTTGAGAT CCTTTTTTTC TGCGCGTAAT CTGCTGCTTG CAAACAAAAA AACCACCGCT ACCAGCGGTG GTTTGTTTGC CGGATCAAGA
     AGTTTCCTAG AAGAACTCTA GGAAAAAAAG ACGCGCATTA GACGACGAAC GTTTGTTTTT TTGGTGGCGA TGGTCGCCAC CAAACAAACG GCCTAGTTCT

                                                                       sau3AI
                                                                       mboI/ndeII[dam-]
                                                                       dpnI[dam+]
                                                                       dpnII[dam-]
                                                                       alwI[dam-]

                                                                  rmaI
                          bsrI            hinPI                   maeI                haeIII/palI
                       maeIII    eco57I   hhaI/cfoI               bfaI      bslI     haeI
7201 GCTACCAACT CTTTTTCCGA AGGTAACTGG CTTCAGCAGA GCGCAGATAC CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA CTTCAAGAAC
     CGATGGTTGA GAAAAAGGCT TCCATTGACC GAAGTCGTCT CGCGTCTATG GTTTATGACA GGAAGATCAC ATCGGCATCA ATCCGGTGGT GAAGTTCTTG

                                                      fnu4HI
                                                      bsoFI                          scrFI
                                                      bbvI                           nciI
                                                   fnu4HI                            mspI
                                               alwNI[dcm-]                           hpaII
                                              bsrI   bsoFI                           dsaV      pleI
 scfI    aciI        mnlI              maeIII     bbvI      bsrI                     cauII     hinfI
7301 TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC TGCTGCCAGT GGCGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT
     AGACATCGTG GCGGATGTAT GGAGCGAGAC GATTAGGACA ATGGTCACCG ACGACGGTCA CCGCTATTCA GCACAGAATG GCCCAACCTG AGTTCTGCTA

                        aciI
                       nspBII                     hgiAI/aspHI
                      fnu4HI                      bsp1286
        mspI          bsoFI                       bsiHKAI
        hpaII         bbvI mcrI                   bmyI
       bsaWI        hinPI  bsiEI                  apaLI/snoI
 maeIII             hhaI/cfoI                     alw44I/snoI  aluI                         ddeI     scfI
7401 AGTTACCGGA TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCGTGCACA CAGCCCAGCT TGGAGCGAAC GACCTACACC GAACTGAGAT ACCTACAGCG
     TCAATGGCCT ATTCCGCGTC GCCAGCCCGA CTTGCCCCCC AAGCACGTGT GTCGGGTCGA ACCTCGCTTG CTGGATGTGG CTTGACTCTA TGGATGTCGC
```

FIG. 48W

```
                                                                                                           scrFI
                                                                                                           mvaI
                                                                                                           ecoRII
                                                              mspI                                         dsaV
           hinPI                                              hpaII  fnu4HI                      bssSI     bstNI
           hhaI/cfoI                                          bslI   bsoFI                     hinPI mnlI  bsaJI
          haeII                            aciI              bsaWI   aciI                      hhaI/cfoI  aluI apyI[dcm+]
7501 TGAGCATTGA GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG GCGGACAGGT ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA
     ACTCGTAACT CTTTCGCGGT GCGAAGGGCT TCCCTCTTTC CGCCTGTCCA TAGGCCATTC GCCGTCCCAG CCTTGTCCTC TCGCGTGCTC CCTCGAAGGT

       scrFI
       mvaI
       ecoRII
       dsaV
       bstNI                                                        taqI                          nlaIV
       apyI[dcm+]                           mnlI drdI            hgaI          sfaNI            aciI
7601 GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG ACTTGAGCGT CGATTTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA
     CCCCCTTTGC GGACCATAGA AATATCAGGA CAGCCCAAAG CGGTGGAGAC TGAACTCGCA GCTAAAAACA CTACGAGCAG TCCCCCCGCC TCGGATACCT

             haeIII/palI        haeIII/palI
           fnu4HI             scrFI
           bsoFI              mvaI bslI
             aciI             ecoRII
          thaI bslI           dsaV                       nlaIII
          fnuDII/mvnI         bstNI          haeIII/palI  nspI
          bstUI               apyI[dcm+]     haeI         nspHI                       tfiI
     cac8I    bsh1236I      nlaIV  haeI   cac8I           aflIII                      hinfI
7701 AAAACGCCAG CAACGCGGCC TTTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTTCTTTCC TGCGTTATCC CCTGATTCTG TGGATAACCG
     TTTTGCGGTC GTTGCGCCGG AAAAATGCCA AGGACCGGAA AACGACCGGA AAACGAGTGT ACAAGAAAGG ACGCAATAGG GGACTAAGAC ACCTATTGGC

                                fnu4HI
                                bsoFI                fnu4HI
                                bbvI                 bsoFI                   sapI   hinPI
                           cac8I aciI                bbvI pleI               mboII hhaI/cfoI
                         bsrBI  fnu4HI       mcrI    hinPI  hinfI            earI/ksp632I
      aciI          aluI  aciI  bsoFI        bsiEI   hhaI/cfoI          mnlI  aciI  haeII
7801 TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCCGCAGC CGAACGACCG AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC AATACGCAAA
     ATAATGGCGG AAACTCACTC GACTATGGCG AGCGGCGTCG GCTTGCTGGC TCGCGTCGCT CAGTCACTCG CTCCTTCGCC TTCTCGCGGG TTATGCGTTT
```

FIG. 48X

```
                 thaI
                 fnuDII/mvnI
                 bstUI
                 bsh1236I
                hinPI
                hhaI/cfoI
               thaI
               fnuDII/mvnI                 cac8I
               bstUI   haeIII/palI        aluI
               bsh1236I         tru9I   pvuII                                                               tru9I
      mnlI     bslI     eaeI   tfiI aseI/asnI/vspI                              cac8I       hinPI        mseI      maeIII
     aciI      aciI     cfrI   hinfI mseI   nspBII                      bsrI     aciI        hhaI/cfoI   aseI/asnI/vspI
7901 CCGCCTCTCC CCGCGCGTTG GCCGATTCAT TAATCCAGCT GGCACGACAG GTTTCCCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT
     GGCGGAGAGG GGCGCGCAAC CGGCTAAGTA ATTAGGTCGA CCGTGCTGTC CAAAGGGCTG ACCTTTCGCC CGTCACTCGC GTTGCGTTAA TTACACTCAA

                    scrFI
                    mvaI
                    ecoRII
                    dsaV
                 nlaIV bstNI
                 hgiCI apyI[dcm+]            mspI                        aciI
      mnlI       banI bsaJI                  hpaII                     bsrBI                          aluI
8001 ACCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG CGGATAACAA TTTCACACAG GAAACAGCTA
     TGGAGTGAGT AATCCGTGGG GTCCGAAATG TGAAATACGA AGGCCGAGCA TACAACACAC CTTAACACTC GCCTATTGTT AAAGTGTGTC CTTTGTCGAT
```

FIG. 48Y

```
                    tru9I
                    mseI
                   aseI/asnI/vspI
                  xmnI
          nlaIII  asp700
  8101 TGACCATGAT TACGAATTAA  (SEQ ID NO.68)
       ACTGGTACTA ATGCTTAATT

>length: 8120

aatII(GACGTC):            1690 5947
acc65I(GGTACC):           2969 3967 4529
accI(GTMKAC):             823 1039 2738 4237
aciI(CCGC):               217 229 238 250 260 271 317 422 454 485 574 1385 1795 1871 2248 2250 2758 2982
                          3167 3179 3188 3200 3210 3221 3267 3372 3404 3449 3686 3949 4021 4318 4542 4727
                          4739 4748 4760 4770 4781 4827 4910 4914 5070 5127 5153 5166 5203 5217 5220 5248
                          5275 5680 5699 5741 5751 5790 5979 6026 6125 6234 6311 6355 6476 6522 6713 6804
                          7166 7175 7310 7420 7541 7560 7687 7715 7806 7827 7834 7877 7901 7911 7967 8070
acyI                      see hinlI
aflII/bfrI(CTTAAG):       786
aflIII(ACRYGT):           932 7758
ageI(ACCGGT):             1833
ahaII/bsaHI(GRCGYC):      988 1690 1858 5117 5947 6329
ahaIII/draI(TTTAAA):      696 4935 6290 6982 7001
ahdI/eam1105I(GACNNNNNGTC): 2087 6865
aluI(AGCT):               5 44 332 386 390 753 1097 1165 1370 1431 1951 2603 2751 2784 3282 3336 3340
                          3562 3566 3676 3733 3792 4270 4288 4311 4344 4554 4842 4896 4954 5047 5333 5590
                          5803 5822 6516 6579 6679 7200 7457 7593 7819 7937 8096
alw44I/snoI(GTGCAC):      1876 5651 6198 7444
```

FIG. 48Z

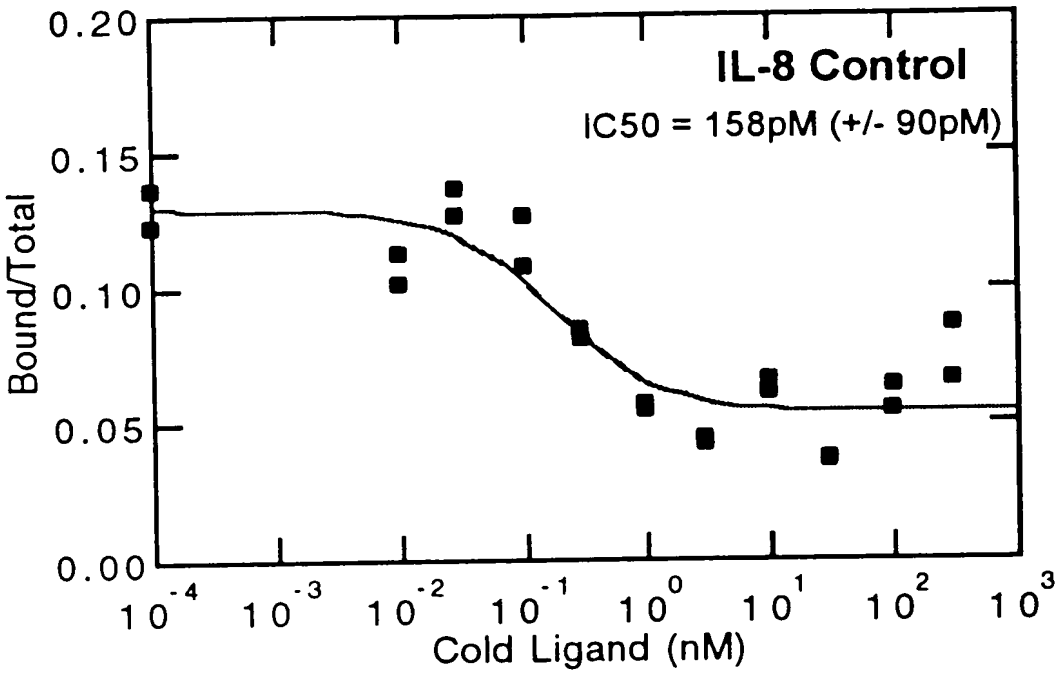


FIG. 49A

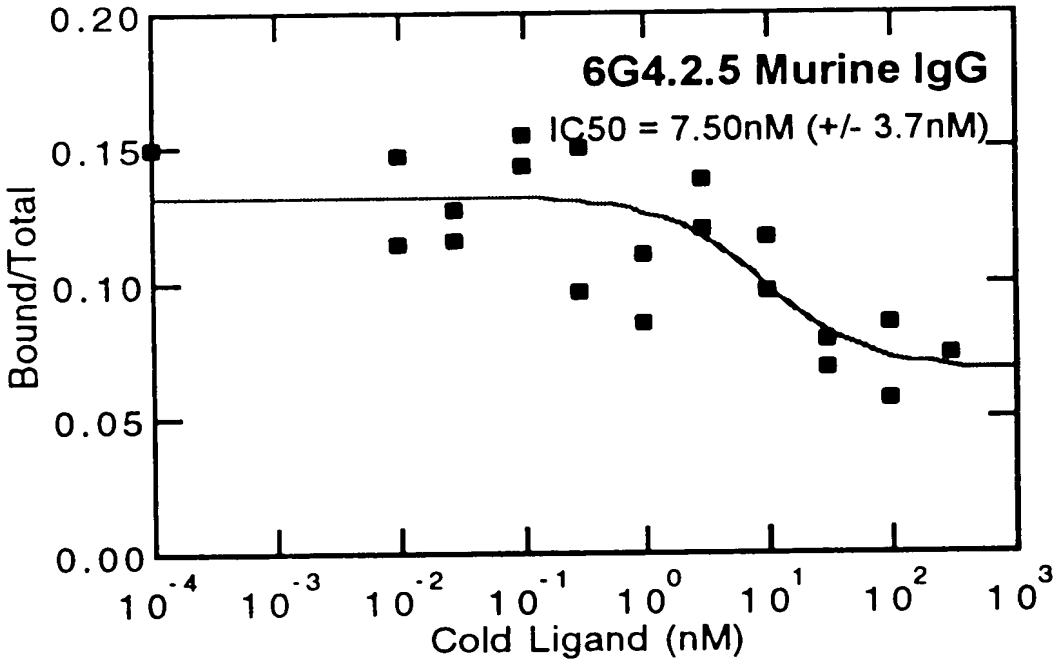


FIG. 49B

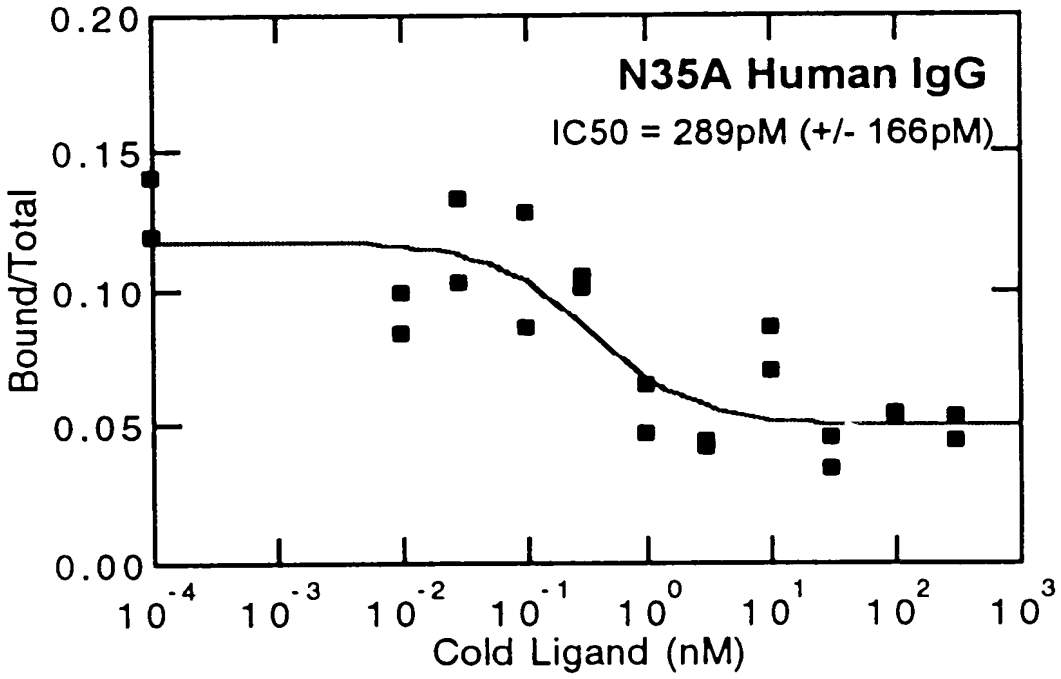


FIG. 49C

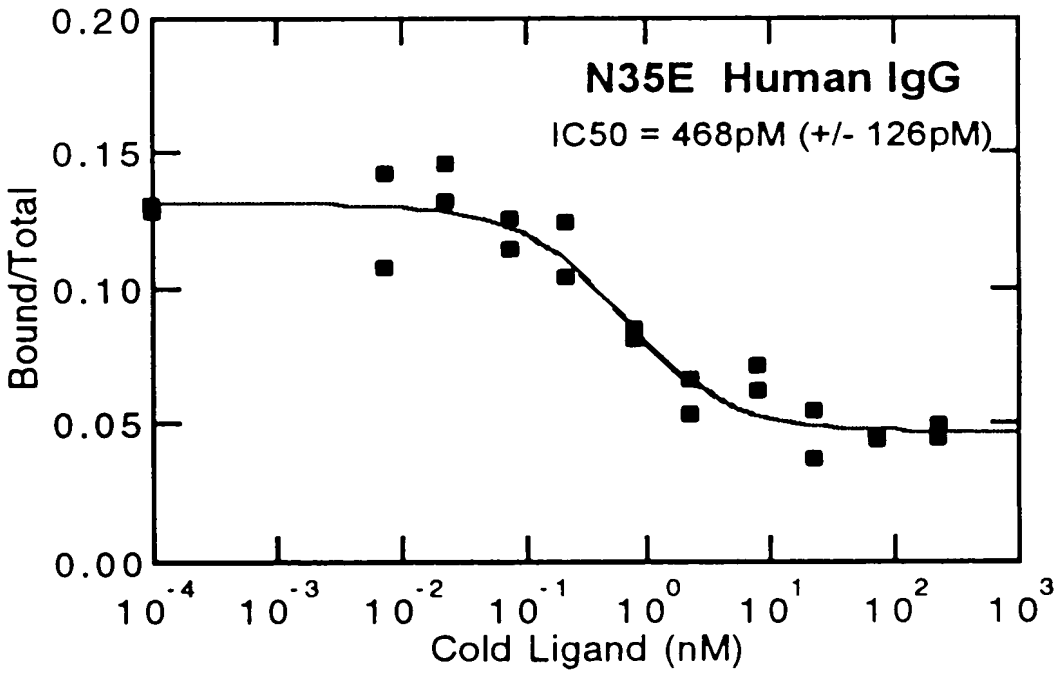


FIG. 49D

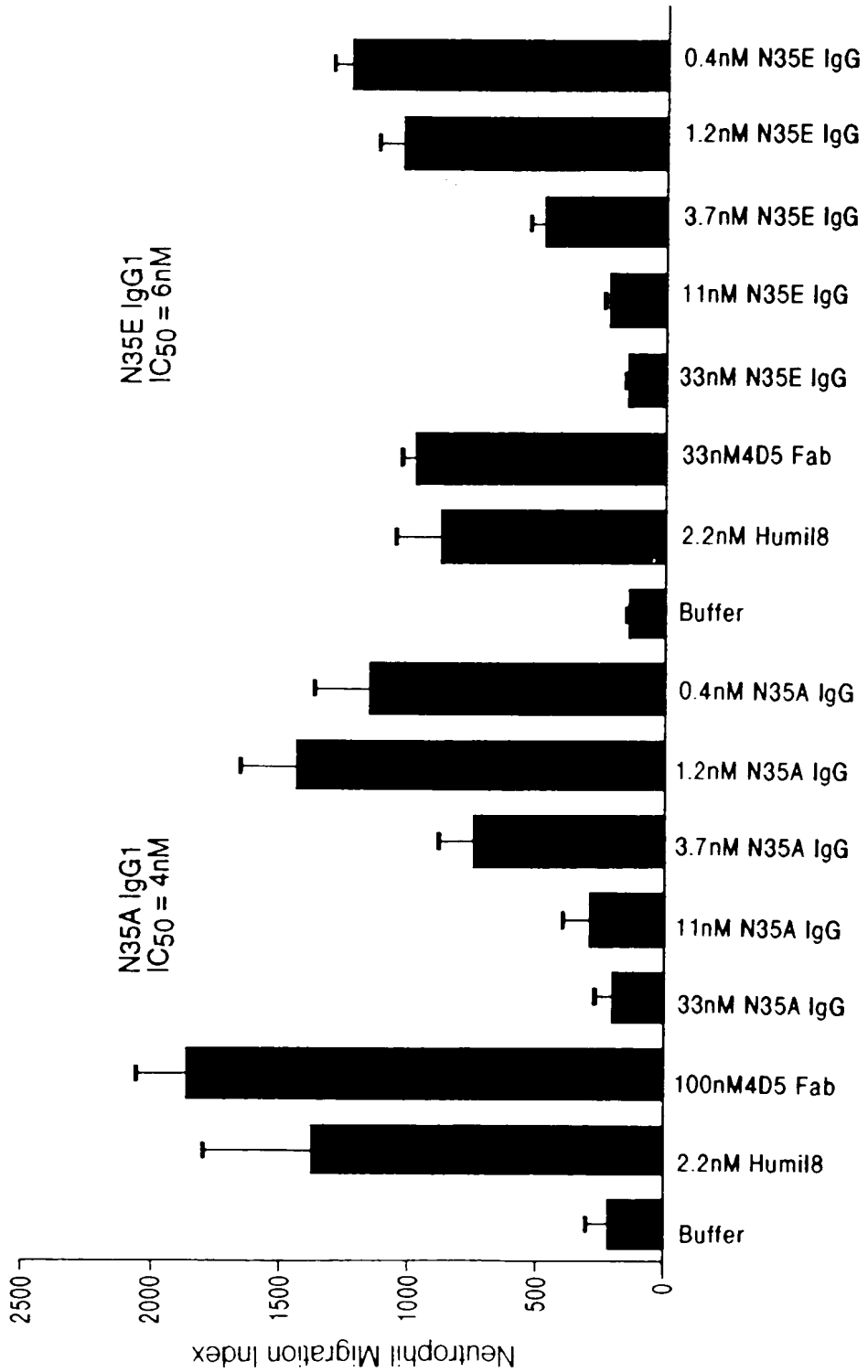


FIG. 50A

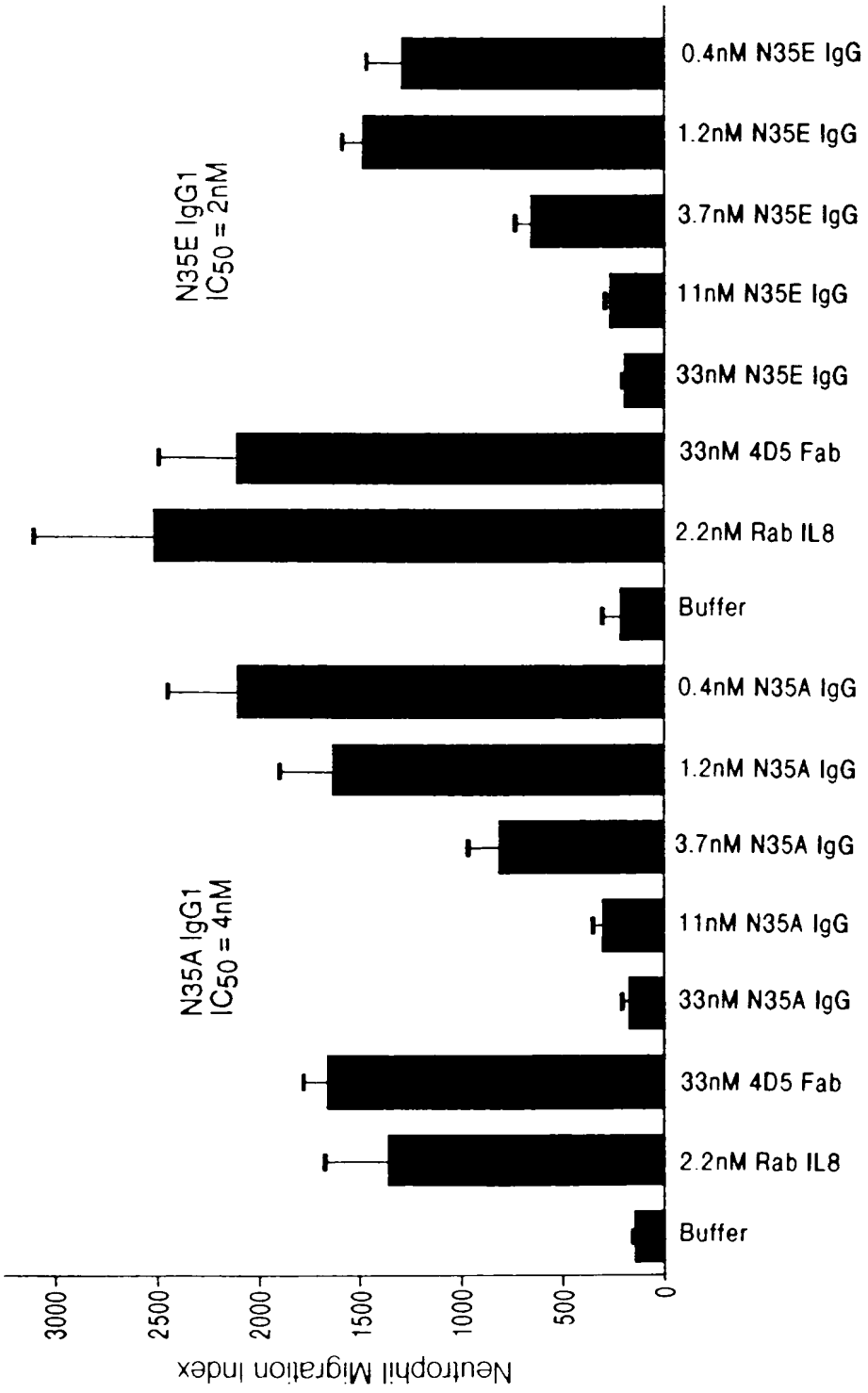
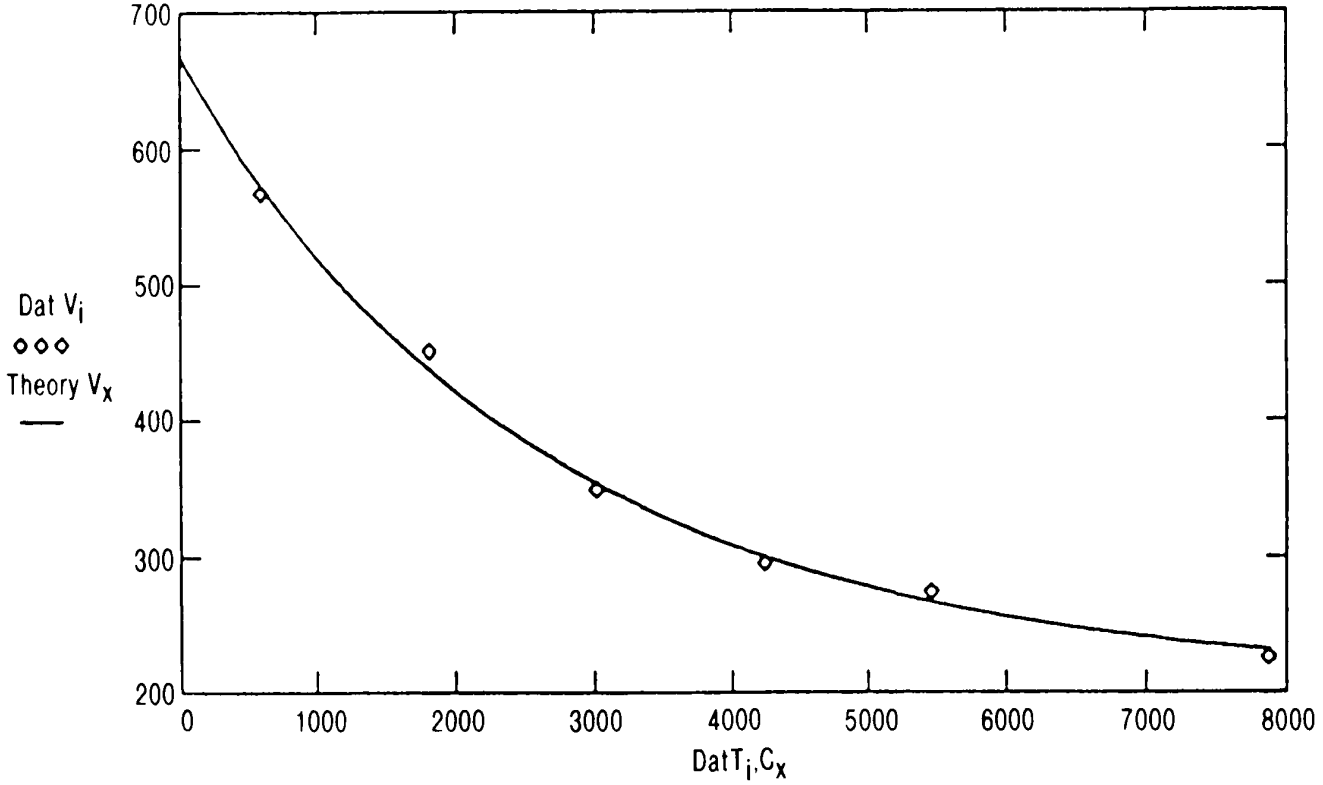


FIG. 50B



Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.IgG1

SAMPLE	ka	kd	Kd
Murine 6G4.2.5 IgG2a	$8.3x10^5$	$2.9x10^{-4}$	350pM
6G4V11N35A-IgG1	$8.7x10^5$	$7.7x10^{-5}$	88pM
6G4V11N35E-IgG1	$3.0x10^6$	$1.4x10^{-4}$	49pM

FIG. 51

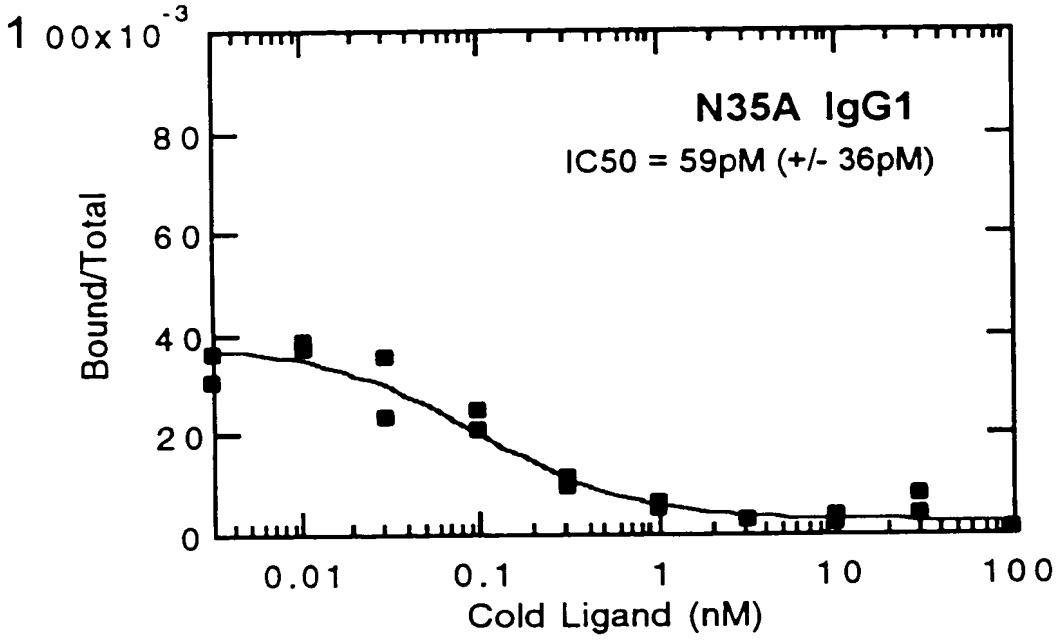


FIG. 52A

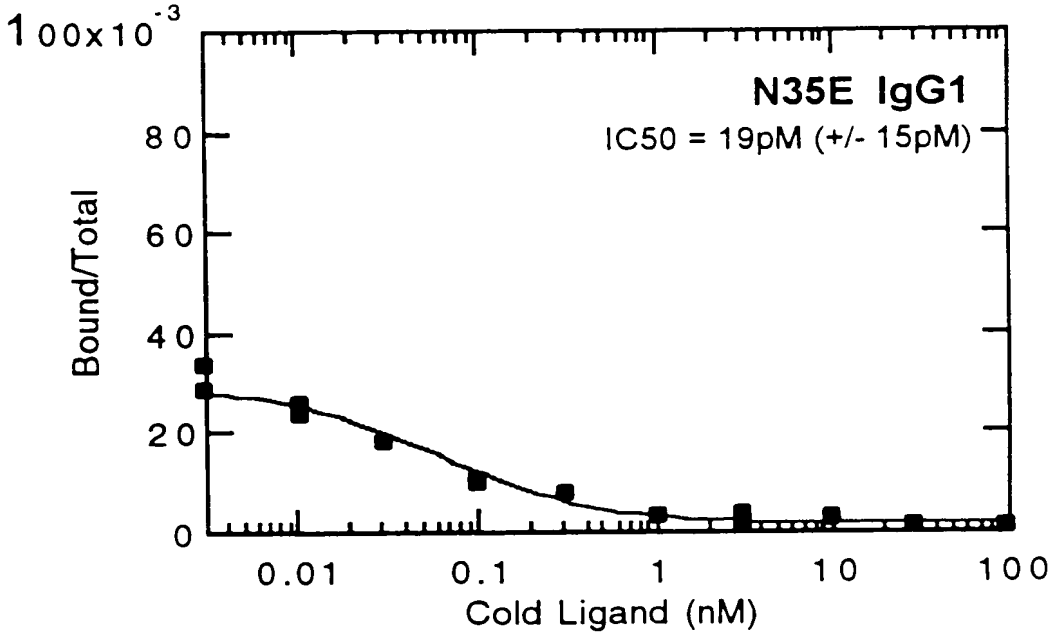


FIG. 52B

```
781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCTTGCA
    TTTTCCCATA GATCTCCAAC TCCACTAAAA TACTTTTTCT TATAGCGTAA AGAAGAACGT
 -1                                   M  K  K  N   I  A  F   L  L  A

841 TCTATGTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG AGGTTCAGCT AGTGCAGTCT
    AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA
-11 S  M  F  V   F  S  I   A  T  N   A  Y  A  E   V  Q  L   V  Q  S

901 GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC
    CCGCCACCGG ACCACGTCGG TCCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG
 8  G  G  G  L   V  Q  P   G  G  S   L  R  L  S   C  A  A   S  G  Y

961 TCCTTCTCGA GTCACTATAT GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG
    AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTCCC GGACCTTACC
 28 S  F  S  S   H  Y  M   H  W  V   R  Q  A  P   G  K  G   L  E  W

1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT
     CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAA GTTCCCGGCA
 48  V  G  Y  I   D  P  S   N  G  E   T  T  Y  N   Q  K  F   K  G  R

1081 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT
     AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA
 68  F  T  L  S   R  D  N   S  K  N   T  A  Y  L   Q  M  N   S  L  R

1141 GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT ATCGCTACAA TGGTGACTGG
     CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCCTAA TAGCGATGTT ACCACTGACC
 88  A  E  D  T   A  V  Y   Y  C  A   R  G  D  Y   R  Y  N   G  D  W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCTC CACCAAGGGC
     AAGAAGCTGC AGACCCCAGT TCCTTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCG
 108 F  F  D  V   W  G  Q   G  T  L   V  T  V  S   S  A  S   T  K  G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG
     GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCCGTG TCGCCGGGAC
 128 P  S  V  F   P  L  A   P  S  S   K  S  T  S   G  G  T   A  A  L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC
     CCGACGGACC AGTTCCTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG
 148 G  C  L  V   K  D  Y   F  P  E   P  V  T  V   S  W  N   S  G  A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC
     GACTGGTCGC CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCCTGA GATGAGGGAG
 168 L  T  S  G   V  H  T   F  P  A   V  L  Q  S   S  G  L   Y  S  L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG
     TCGTCGCACC ACTGGCACGG GAGGTCGTCG AACCCGTGGG TCTGGATGTA GACGTTGCAC
 188 S  S  V  V   T  V  P   S  S  S   L  G  T  Q   T  Y  I   C  N  V

1501 AATCACAAGC CCAGCAACAC CAAGGTCGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA
     TTAGTGTTCG GGTCGTTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT
 208 N  H  K  P   S  N  T   K  V  D   K  K  V  E   P  K  S   C  D  K

1561 ACTCACACAT GCCCGCCGTGA  (SEQ ID NO.69)
     TGAGTGTGTA CGGGCGGCACT
 228 T  H  T  C   P  P  O    (SEQ ID NO.70)
```

FIG. 53

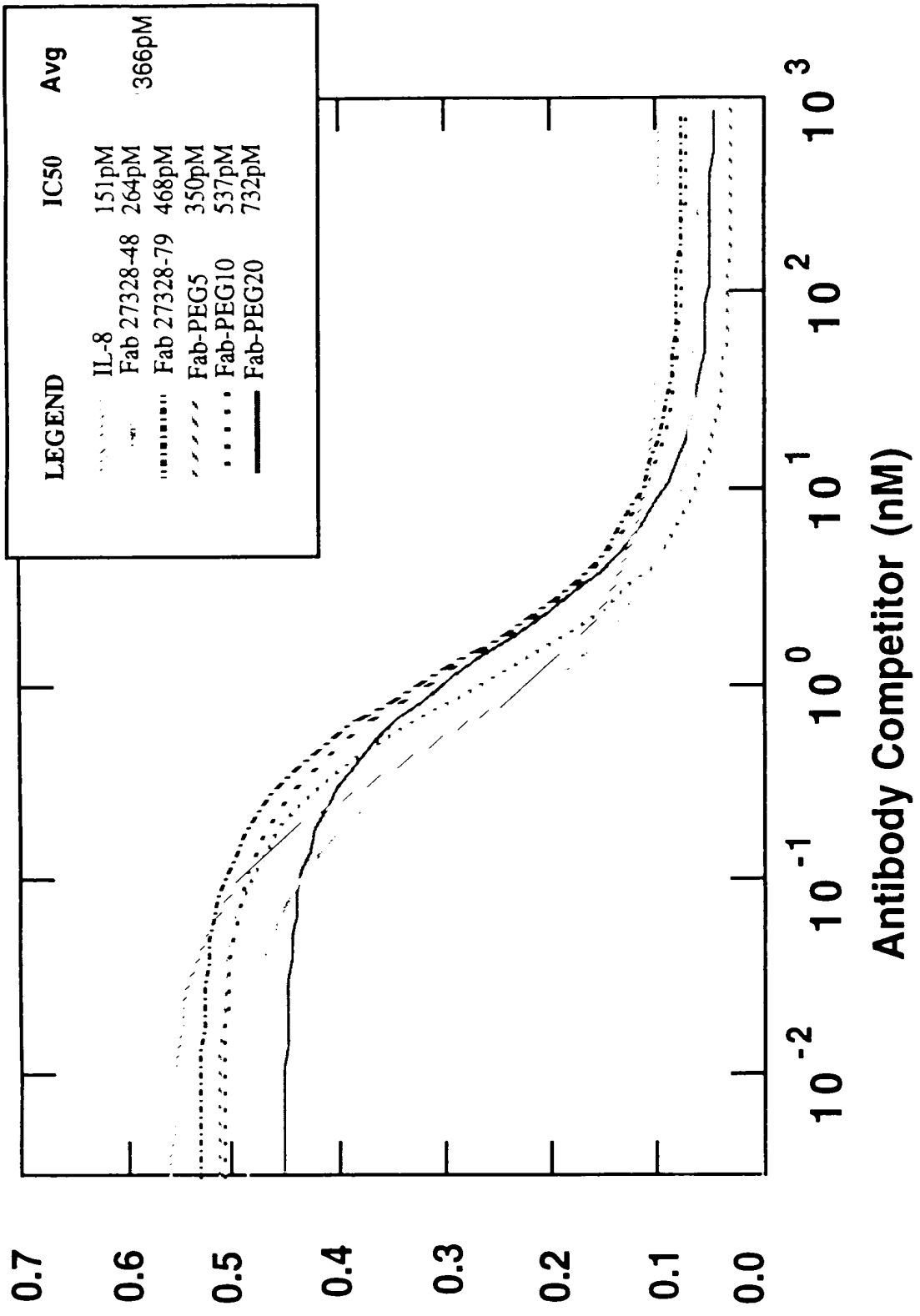


FIG. 54A

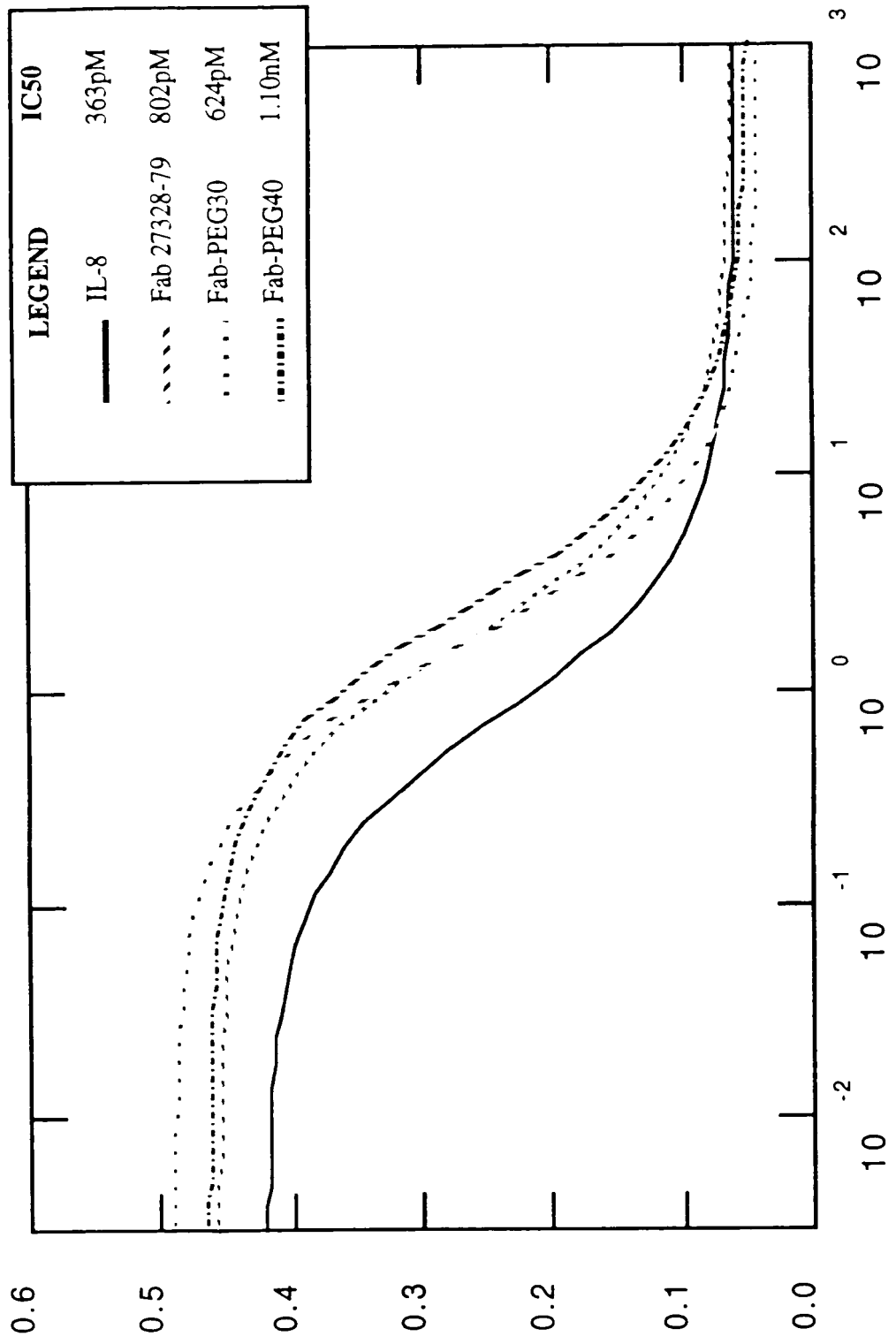


FIG. 54B

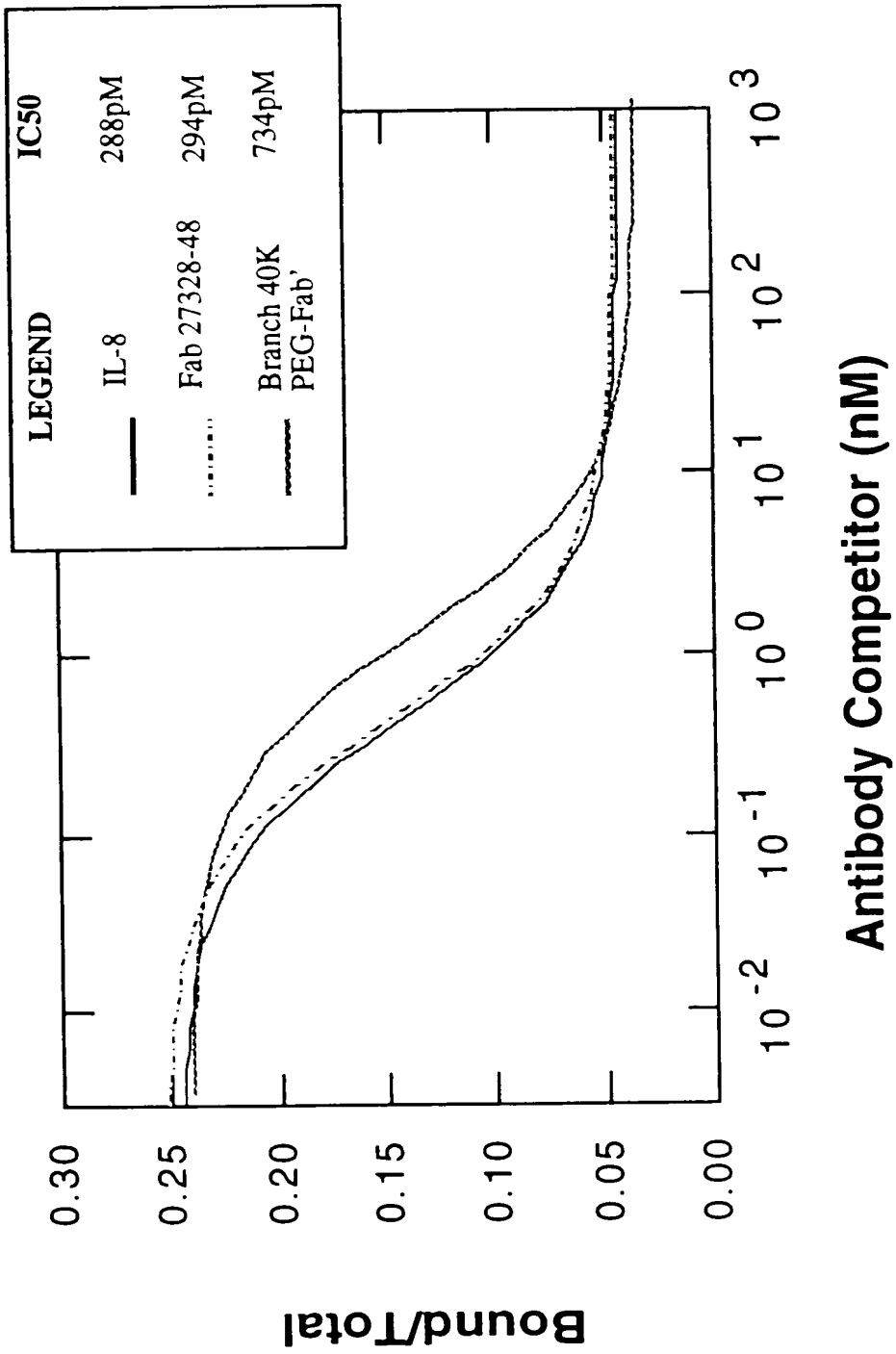


FIG. 54C

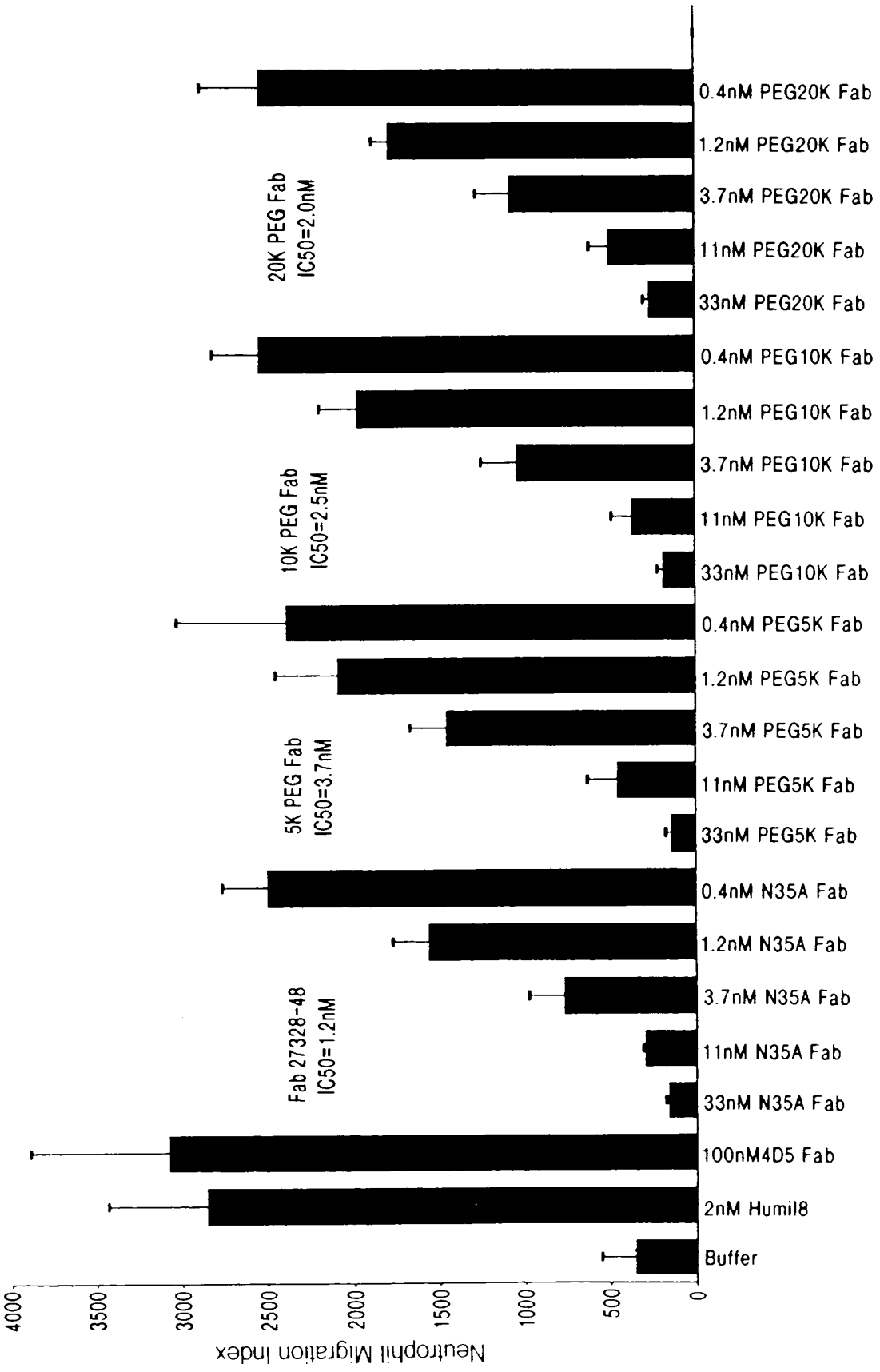


FIG. 55A

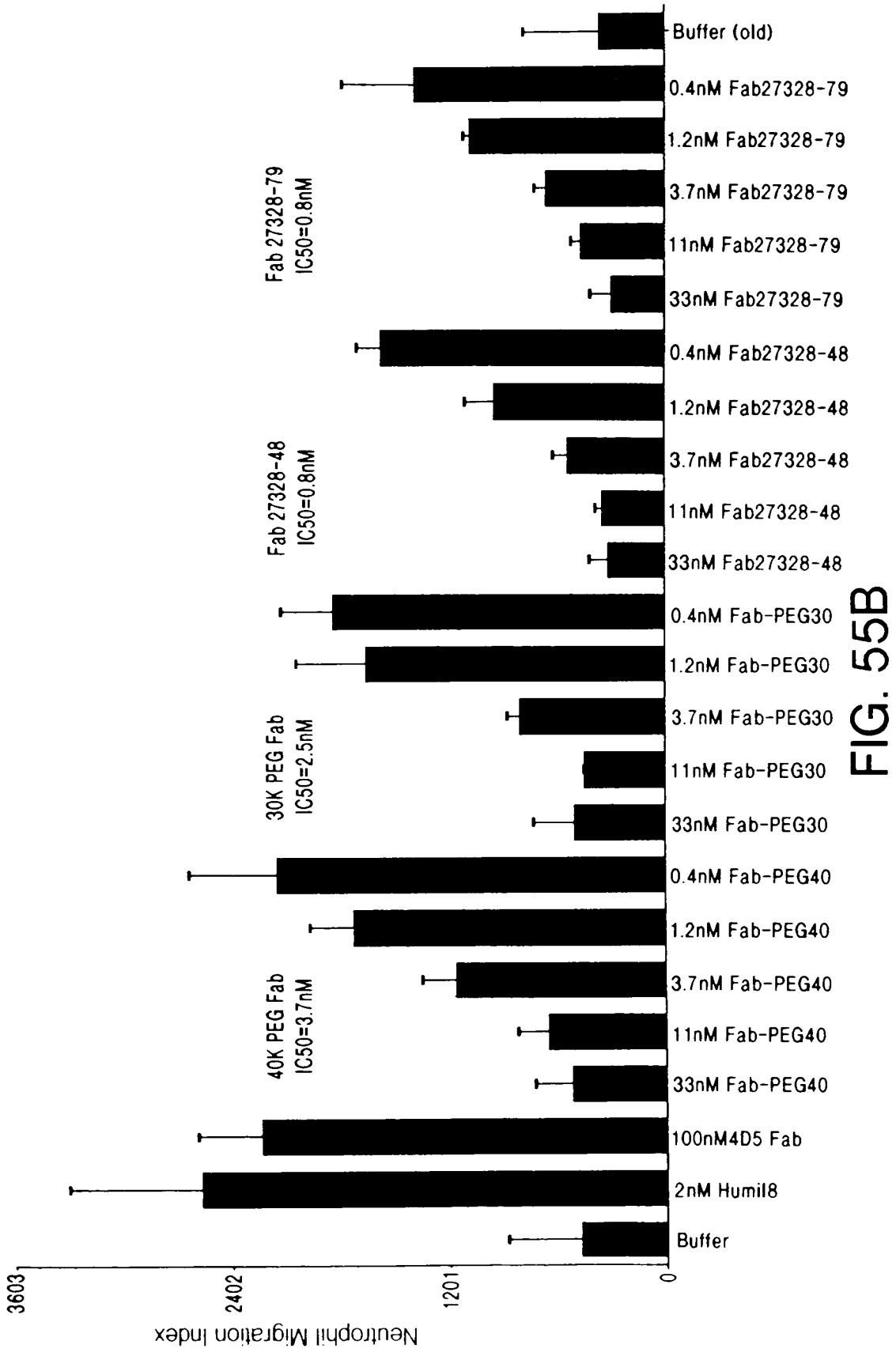


FIG. 55B

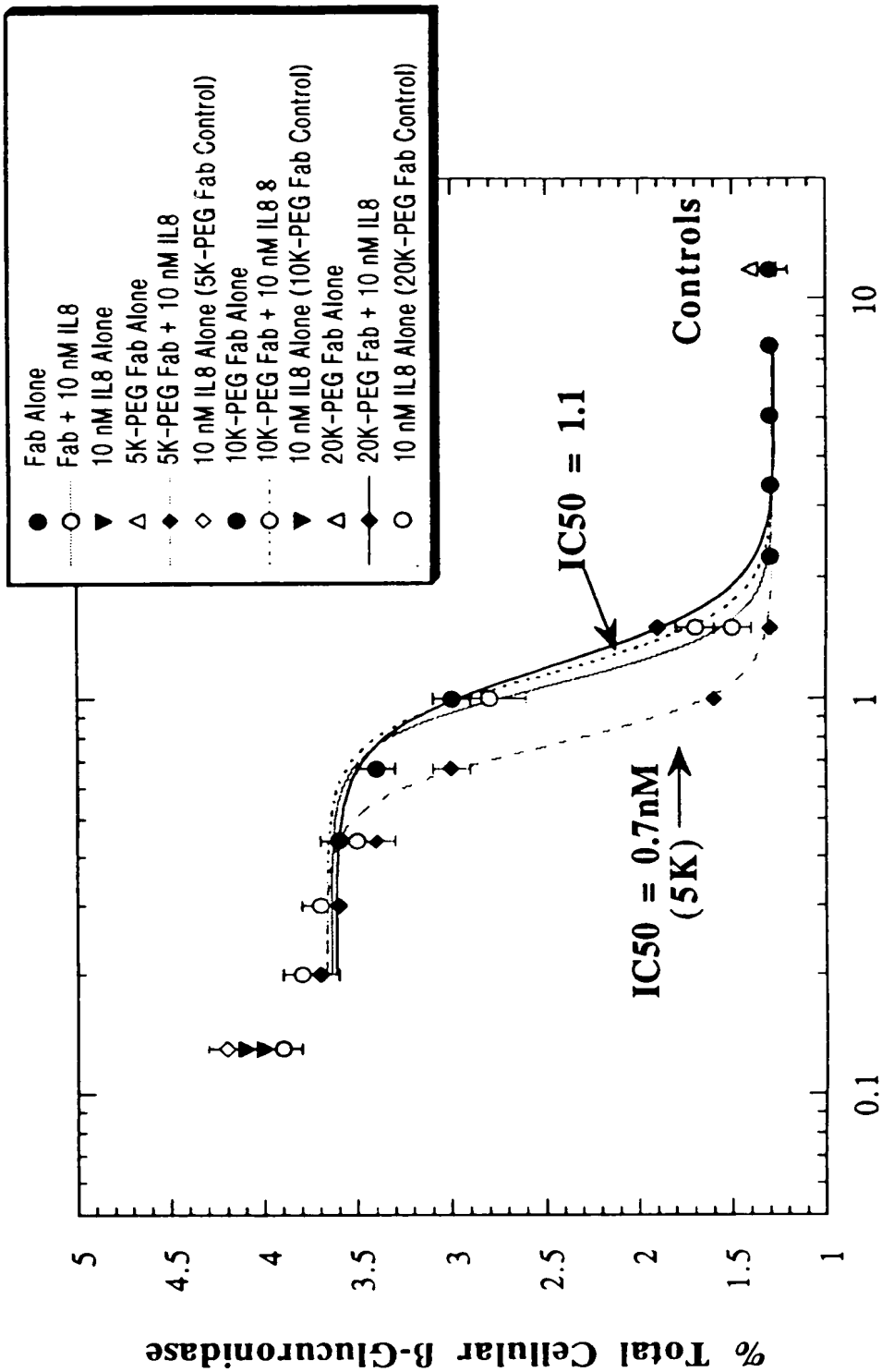

Fab Alone
Fab + 10 nM IL8
10 nM IL8 Alone
5K-PEG Fab Alone
5K-PEG Fab + 10 nM IL8
10 nM IL8 Alone (5K-PEG Fab Control)
10K-PEG Fab Alone
10K-PEG Fab + 10 nM IL8 8
10 nM IL8 Alone (10K-PEG Fab Control)
20K-PEG Fab Alone
20K-PEG Fab + 10 nM IL8
10 nM IL8 Alone (20K-PEG Fab Control)
IC50 = 1.1
Controls
IC50 = 0.7nM
(5K)
% Total Cellular β-Glucuronidase
Molar Ratio Antibody:IL-8
5
4.5
4
3.5
3
2.5
2
1.5
1
0.1
1
10

FIG. 56A

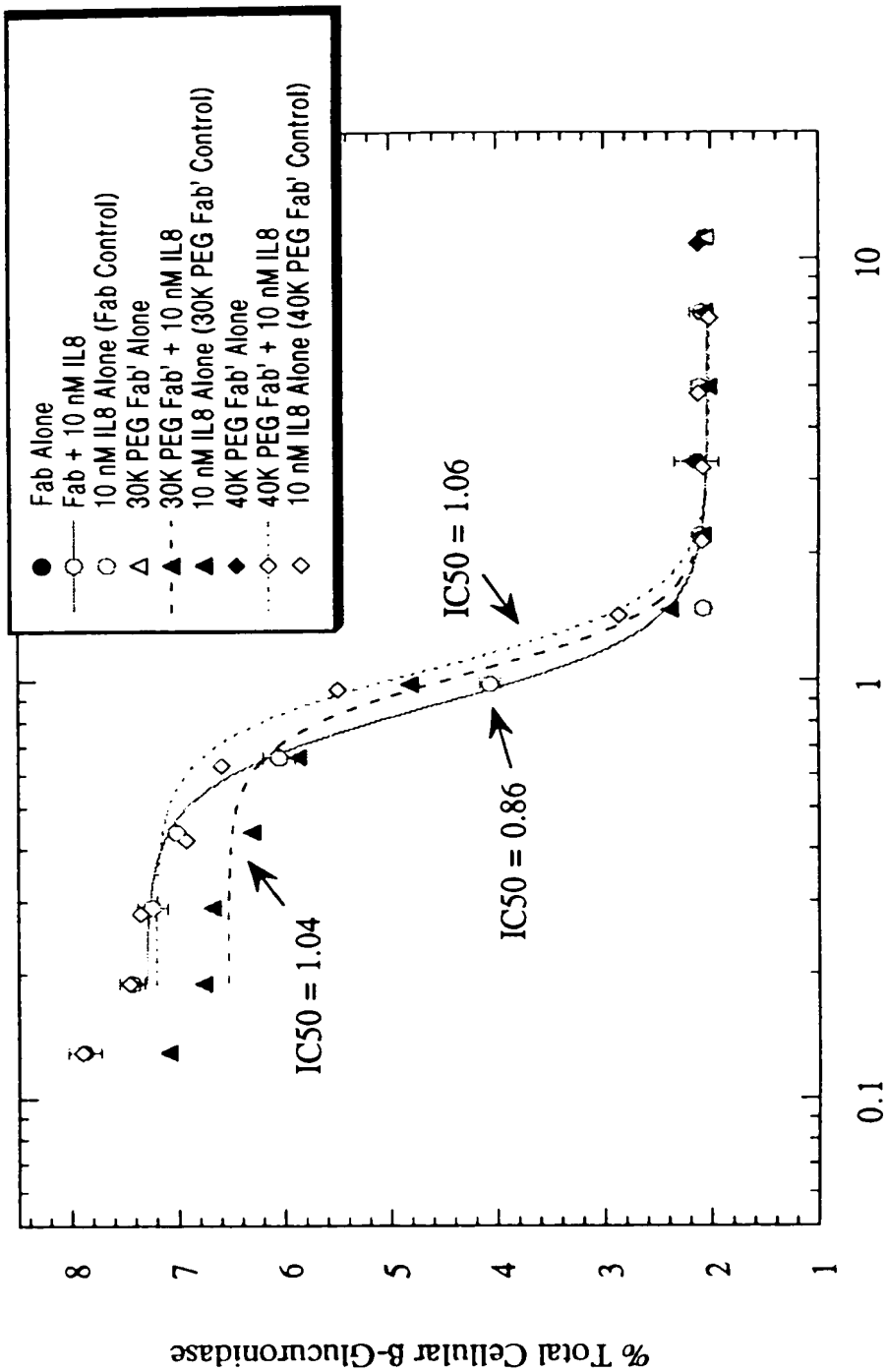


FIG. 56B

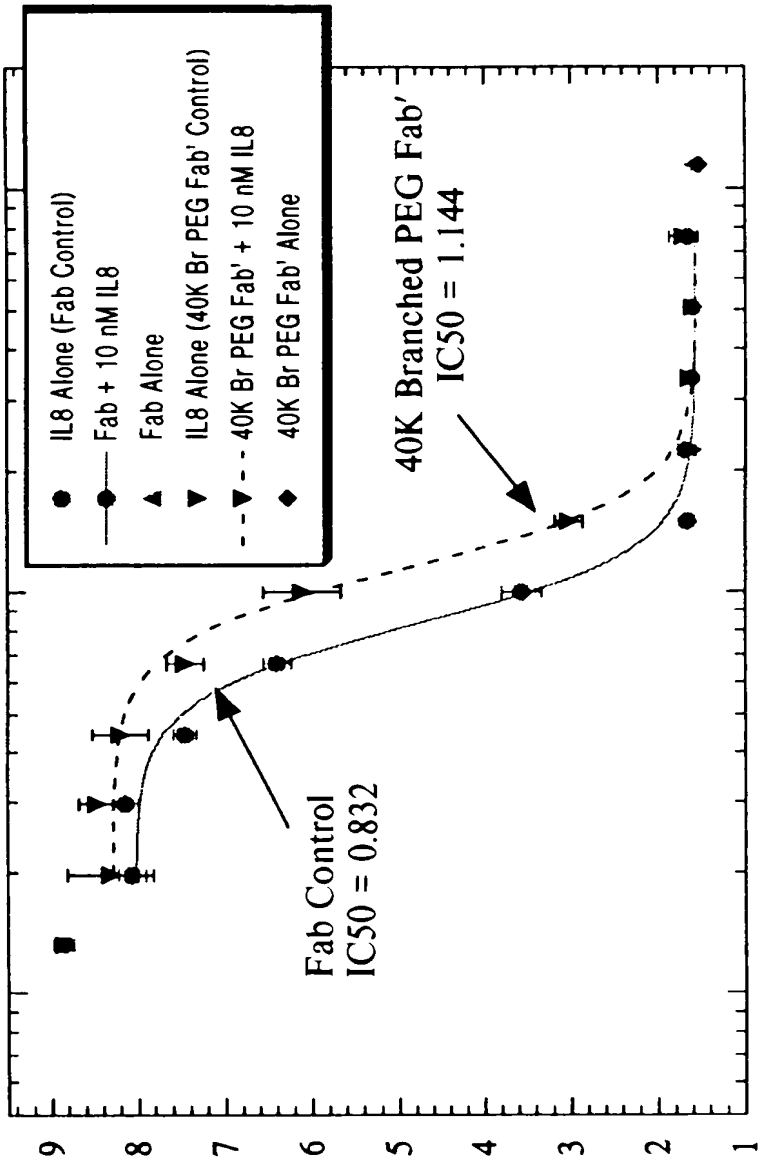


FIG. 56C

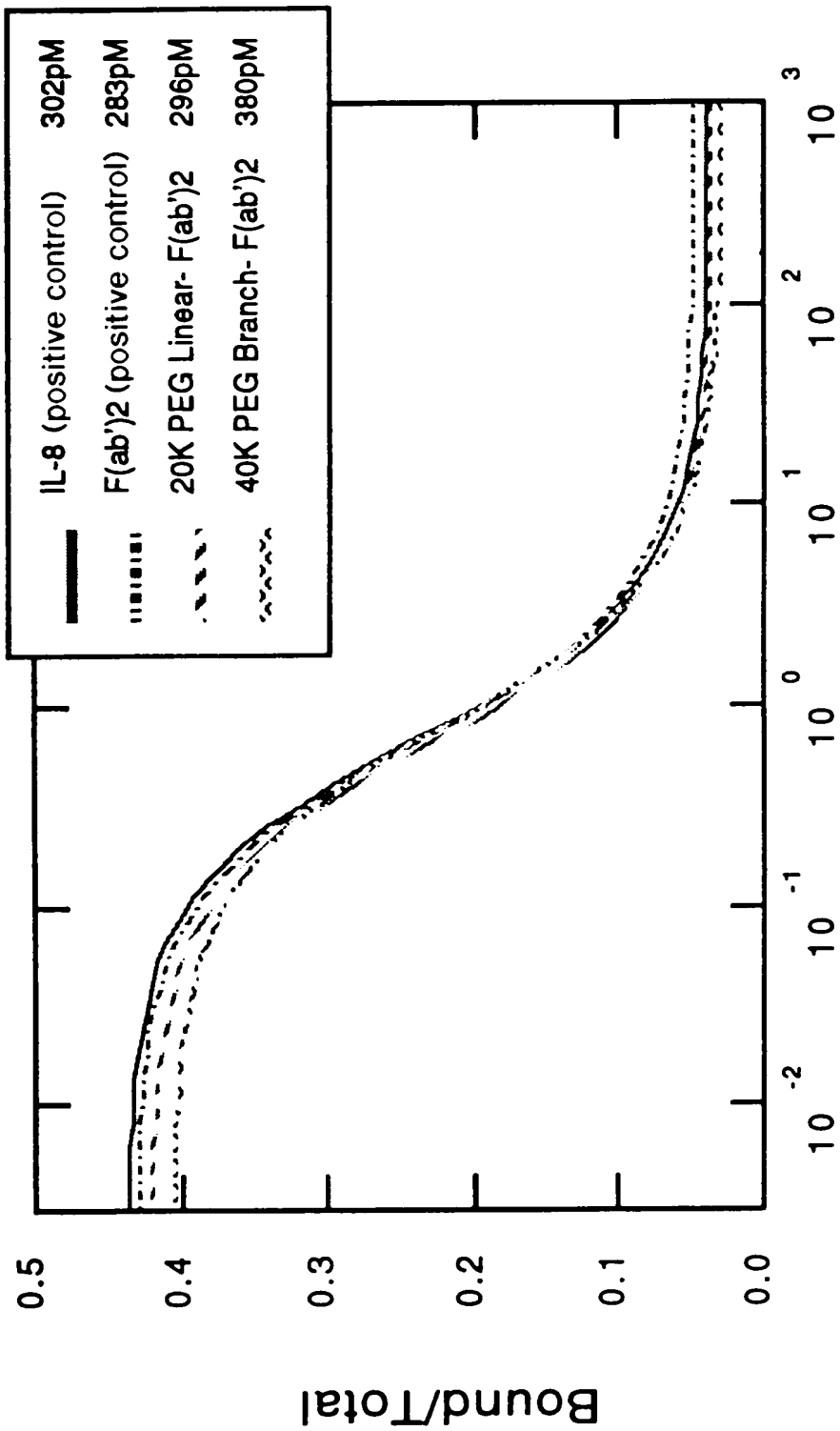


FIG. 57A

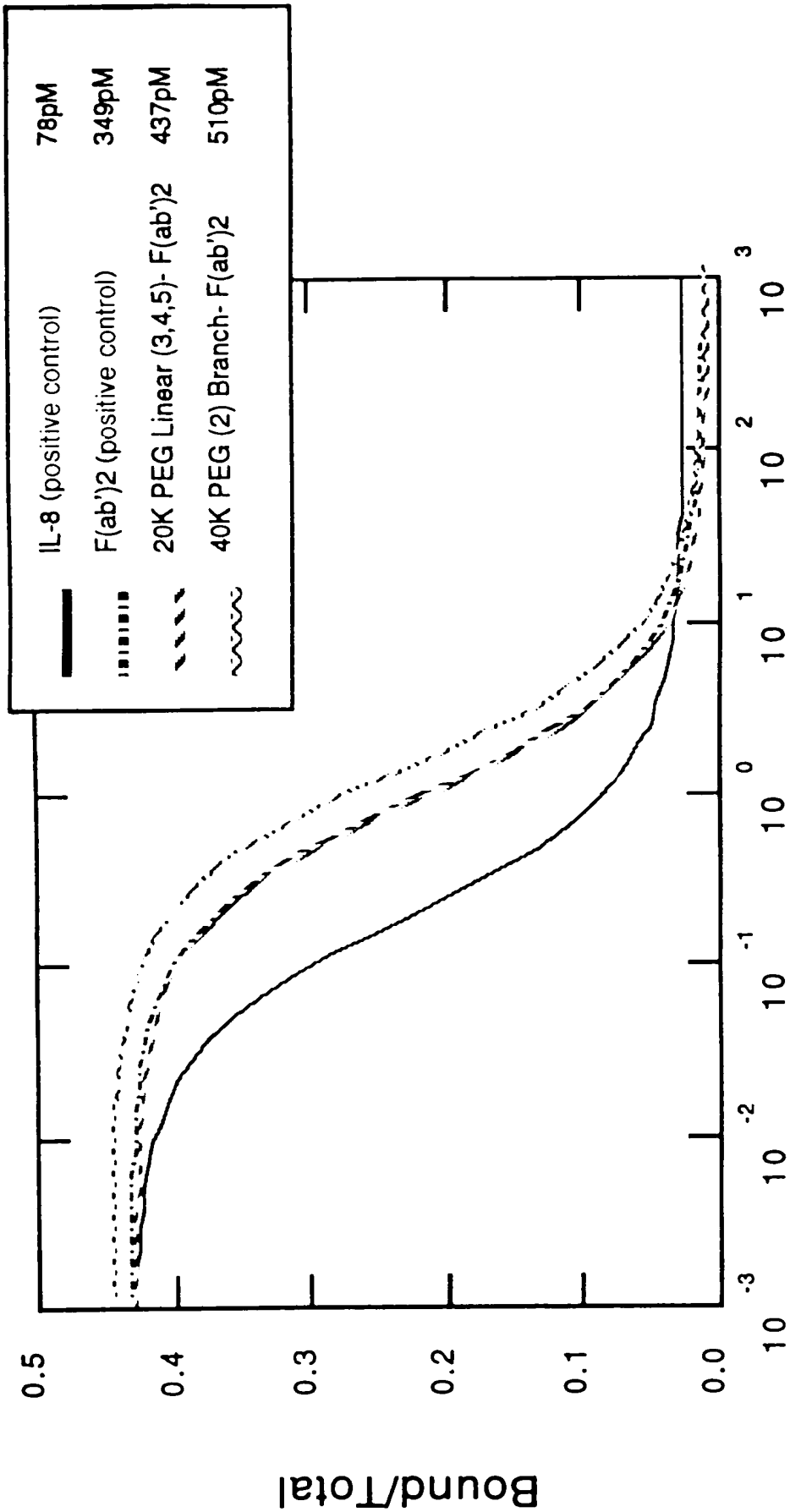


FIG. 57B

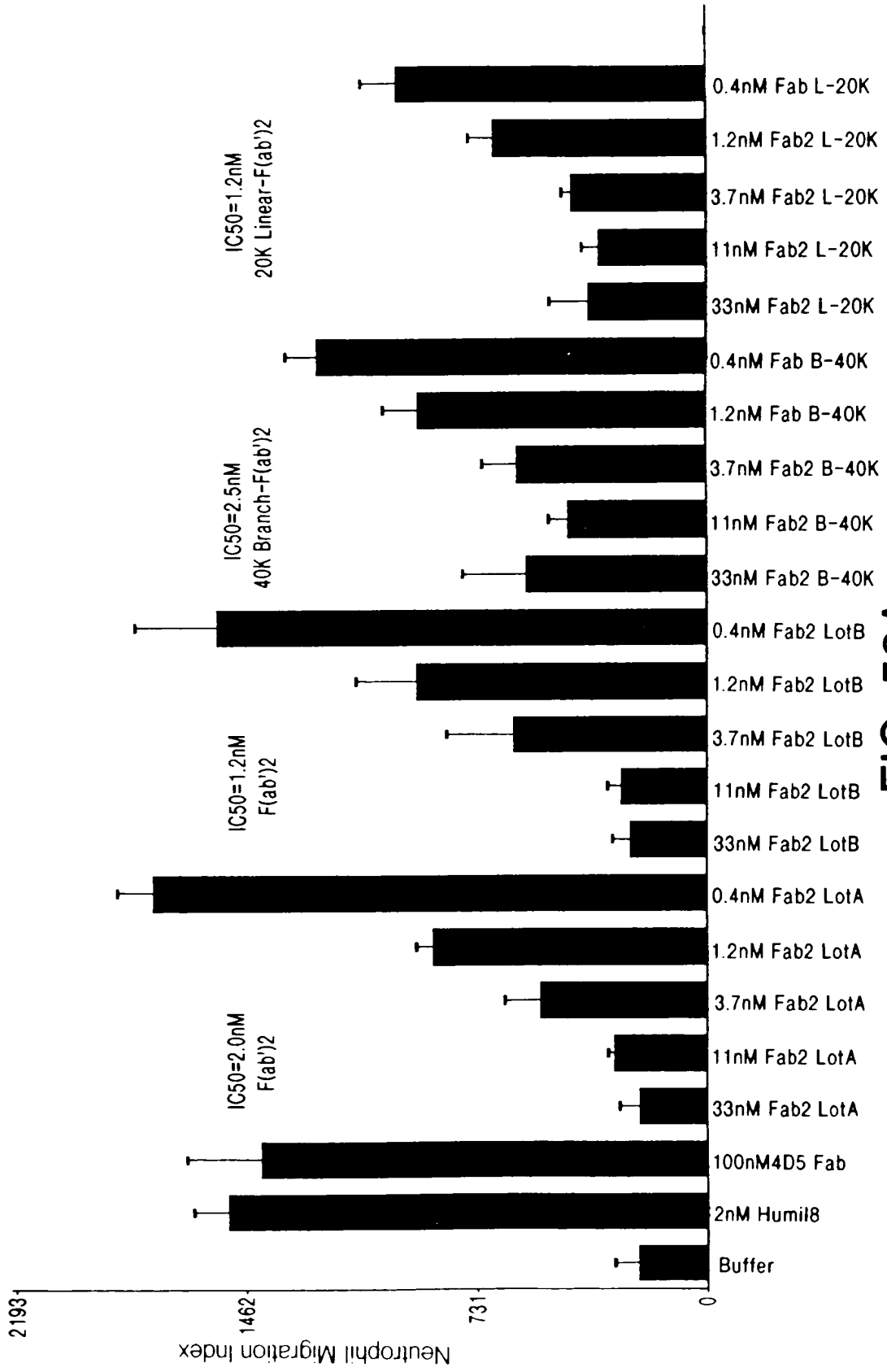


FIG. 58A

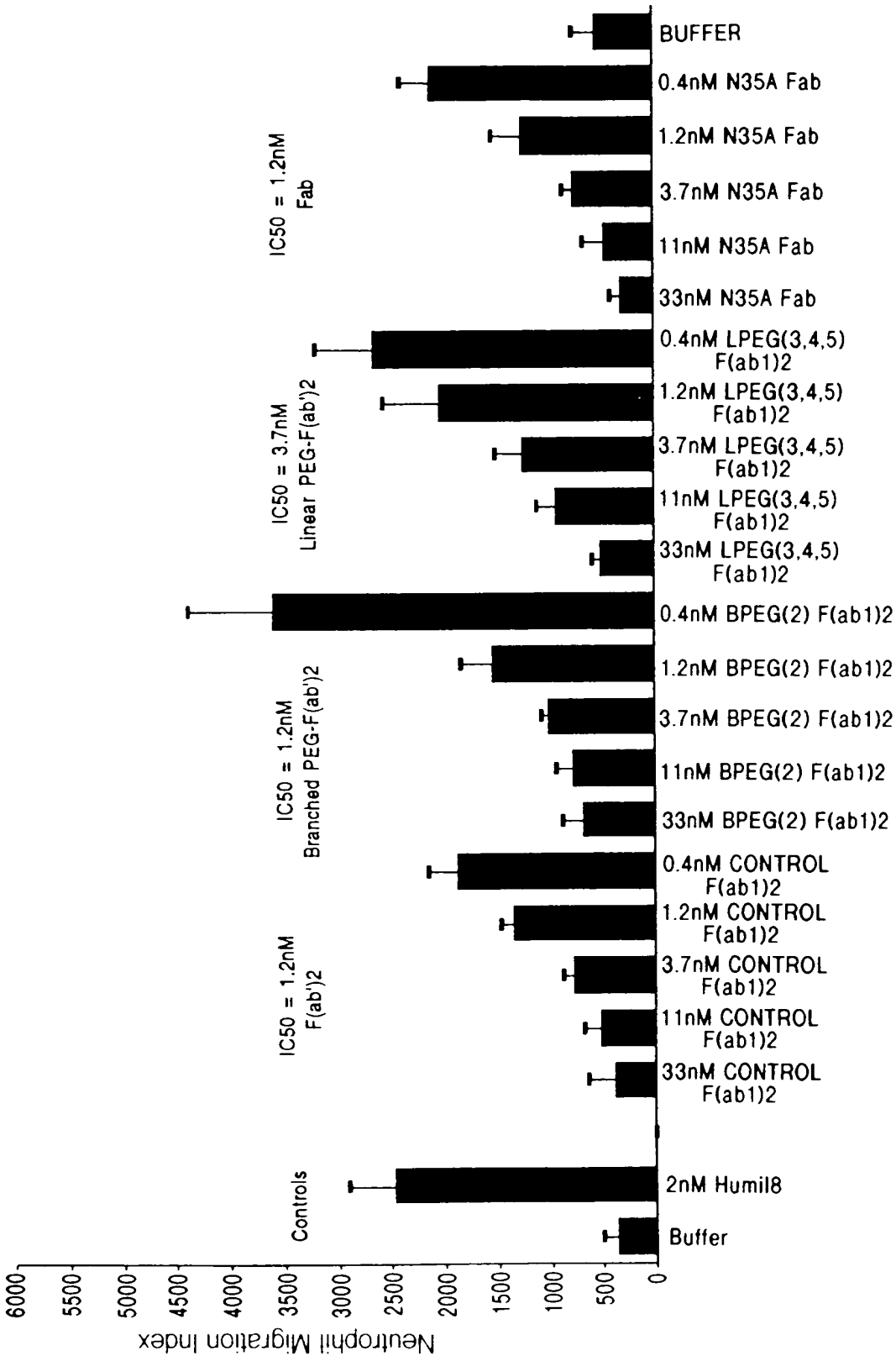


FIG. 58B

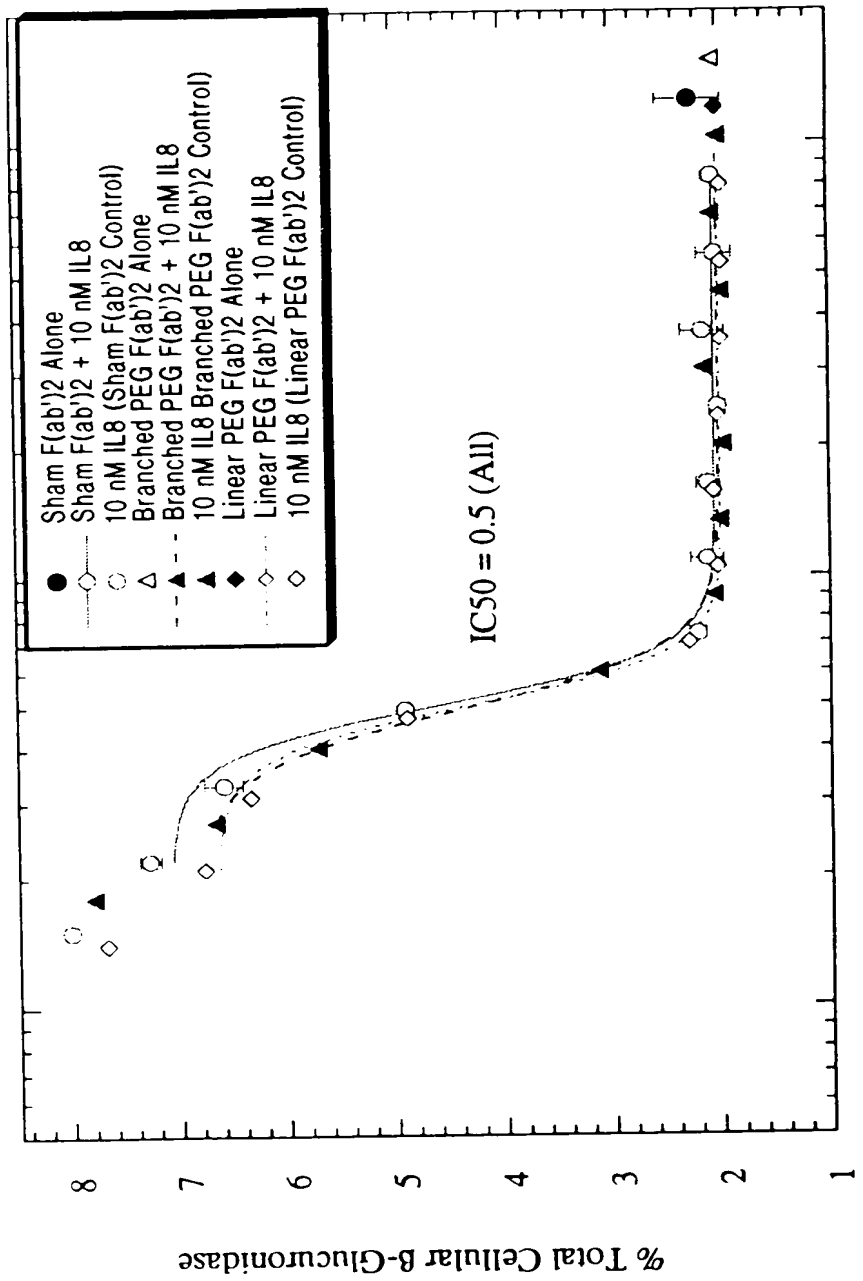


FIG. 59A

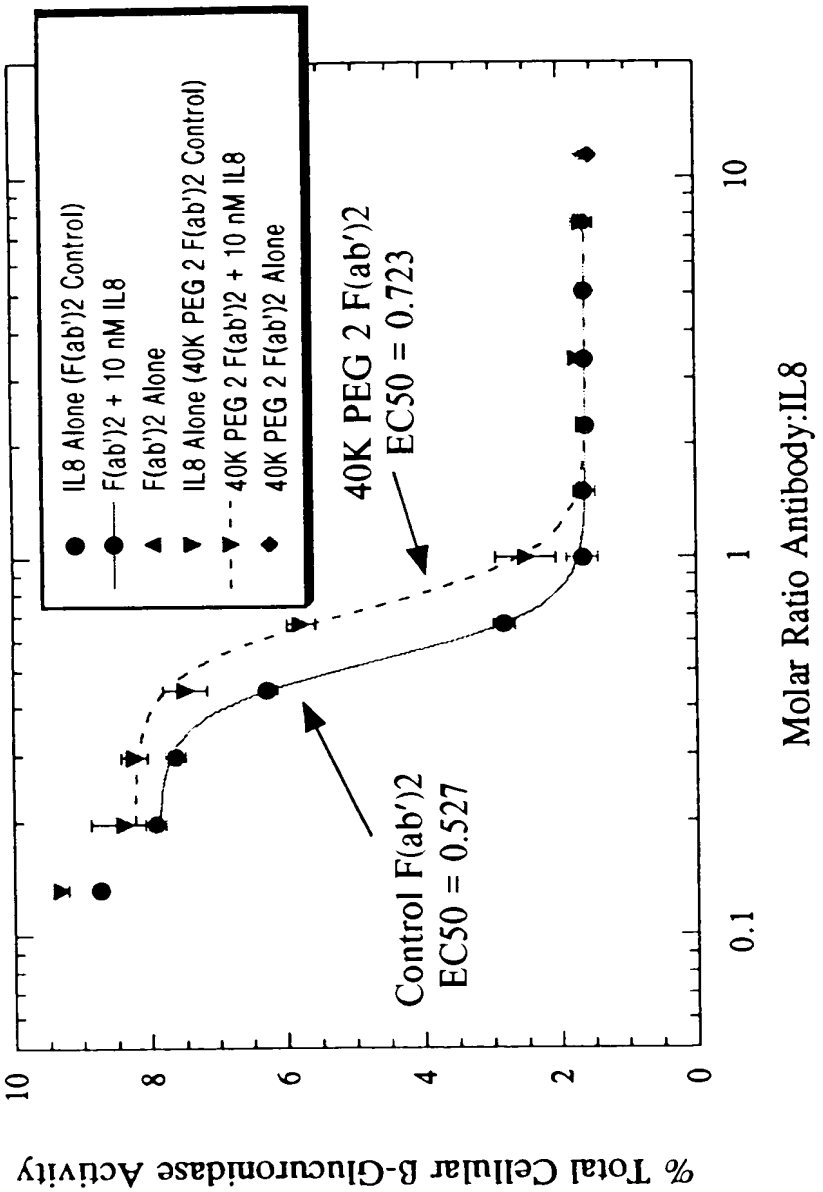


FIG. 59B

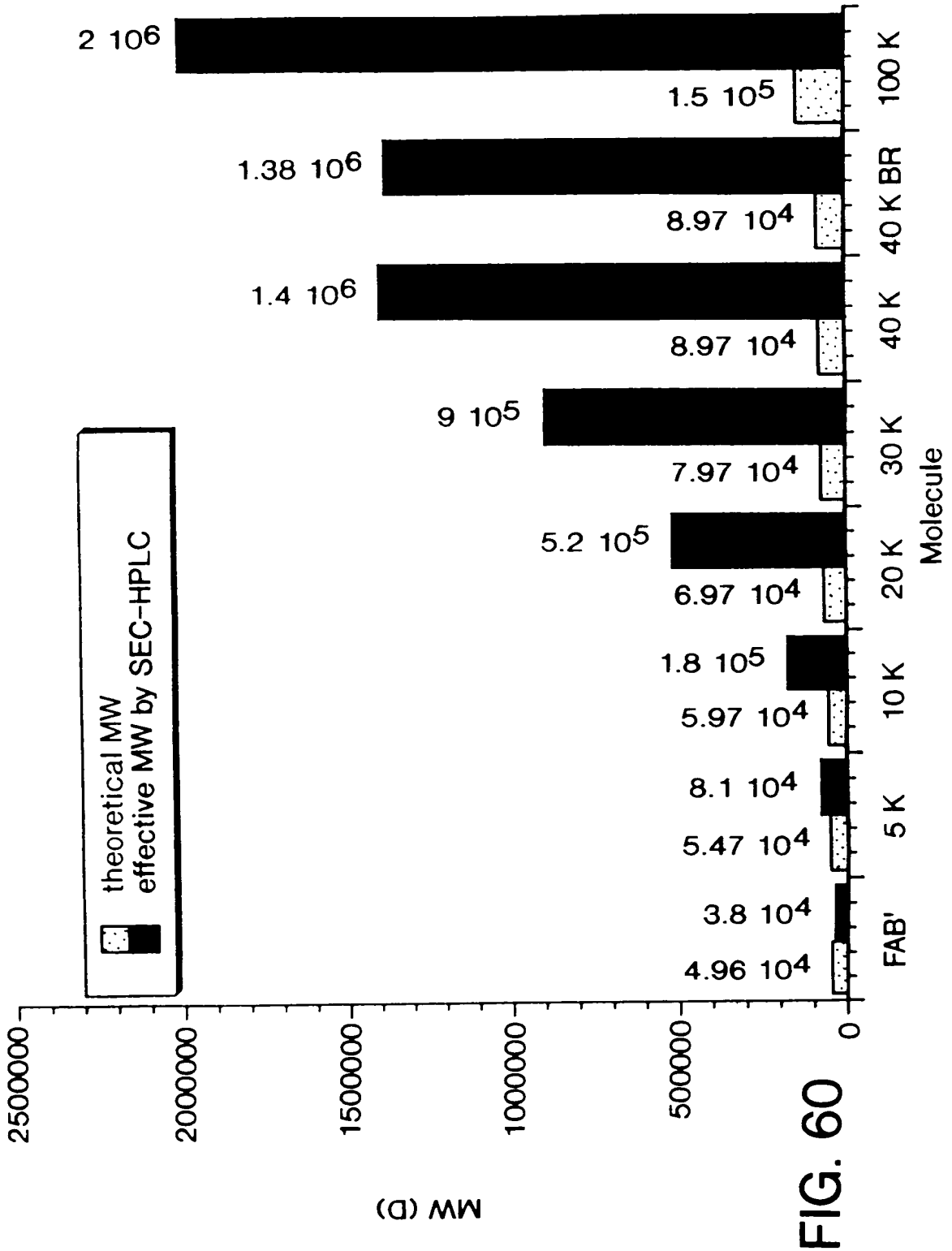


FIG. 60

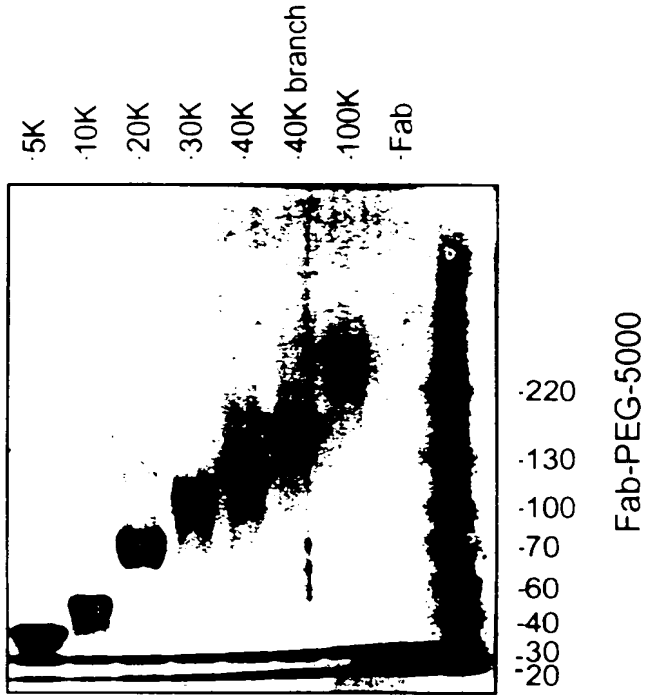


FIG. 61A

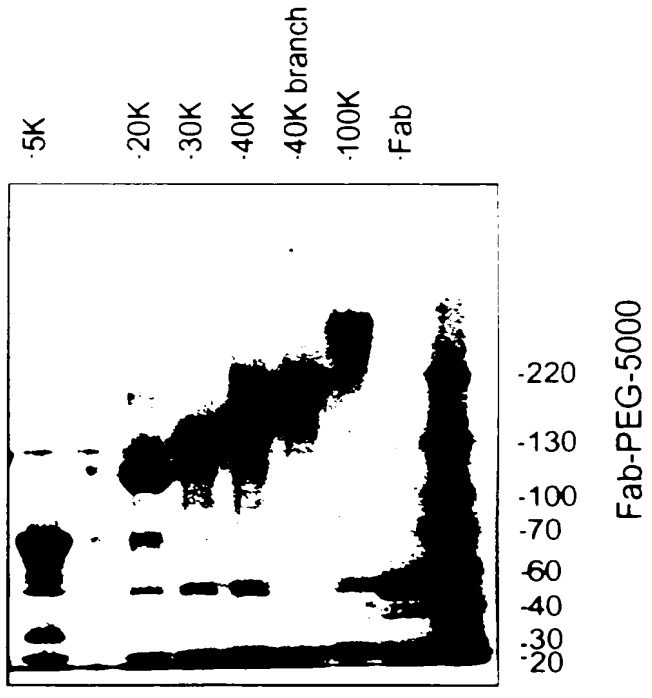


FIG. 61B

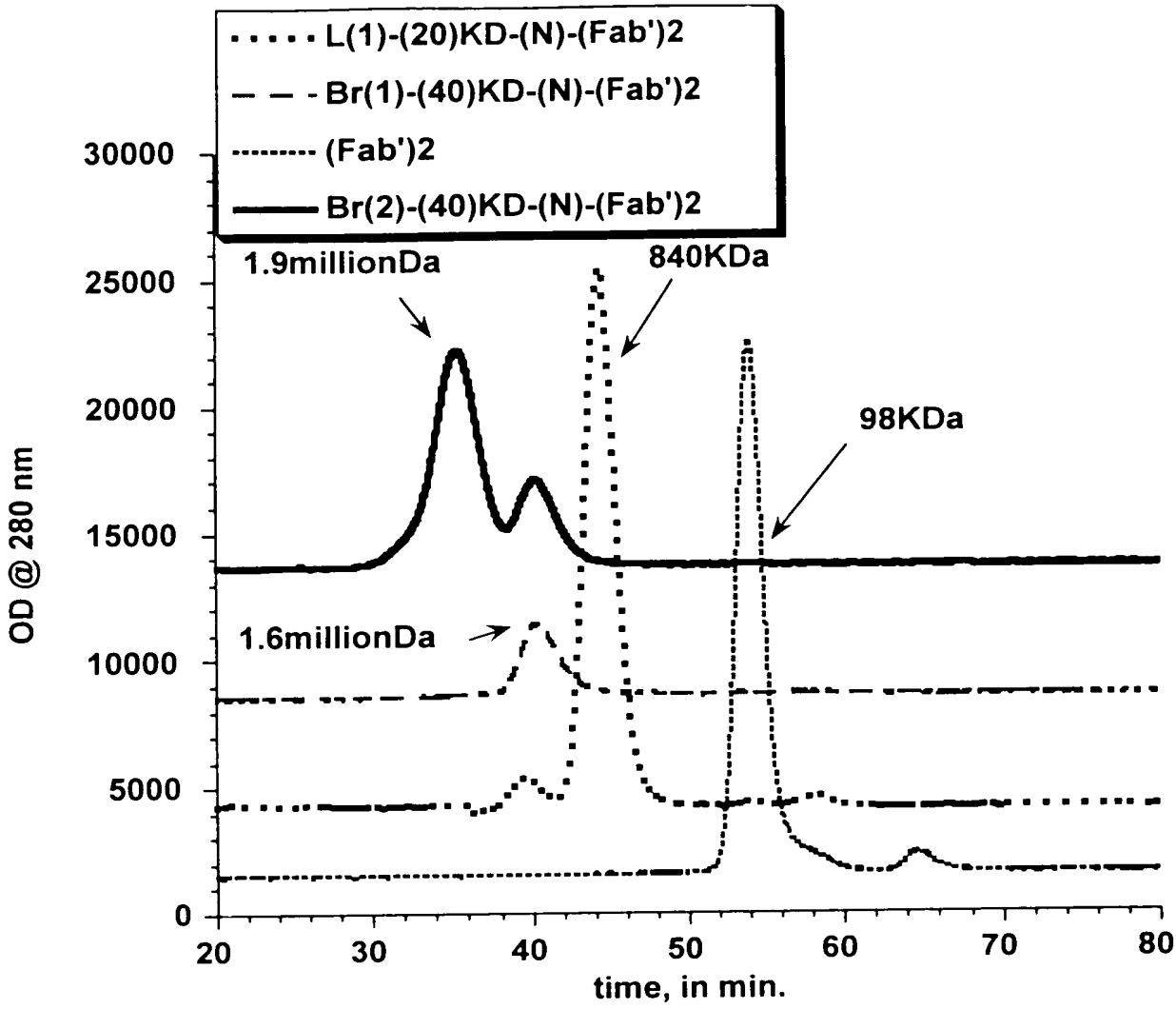


FIG. 62

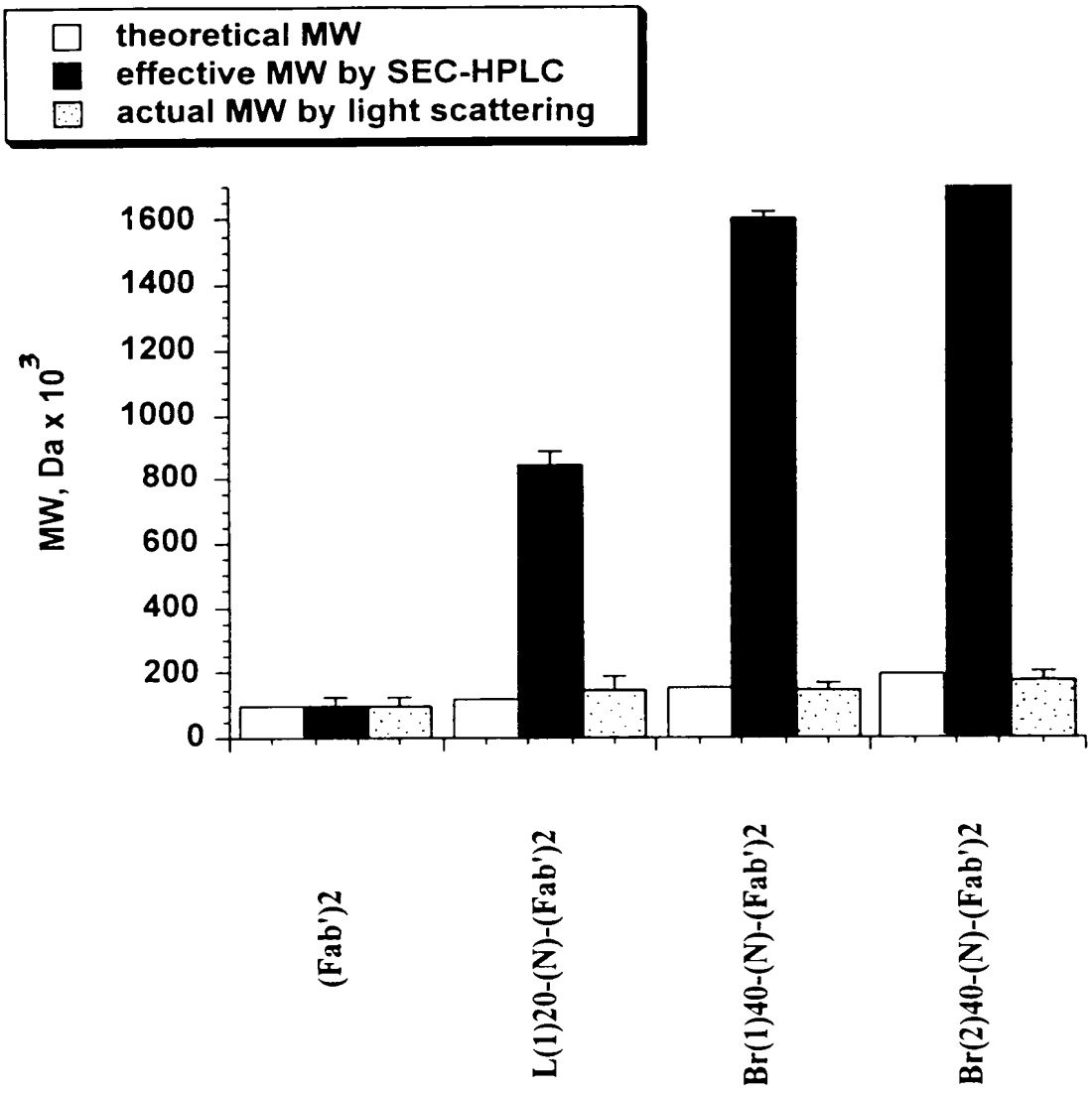


FIG. 63

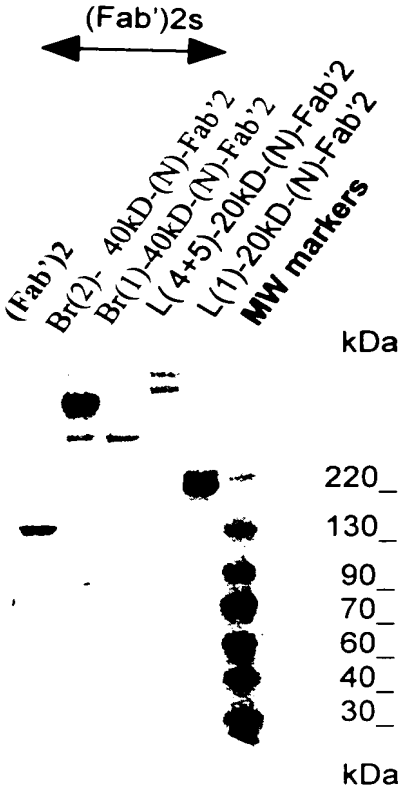


FIG. 64

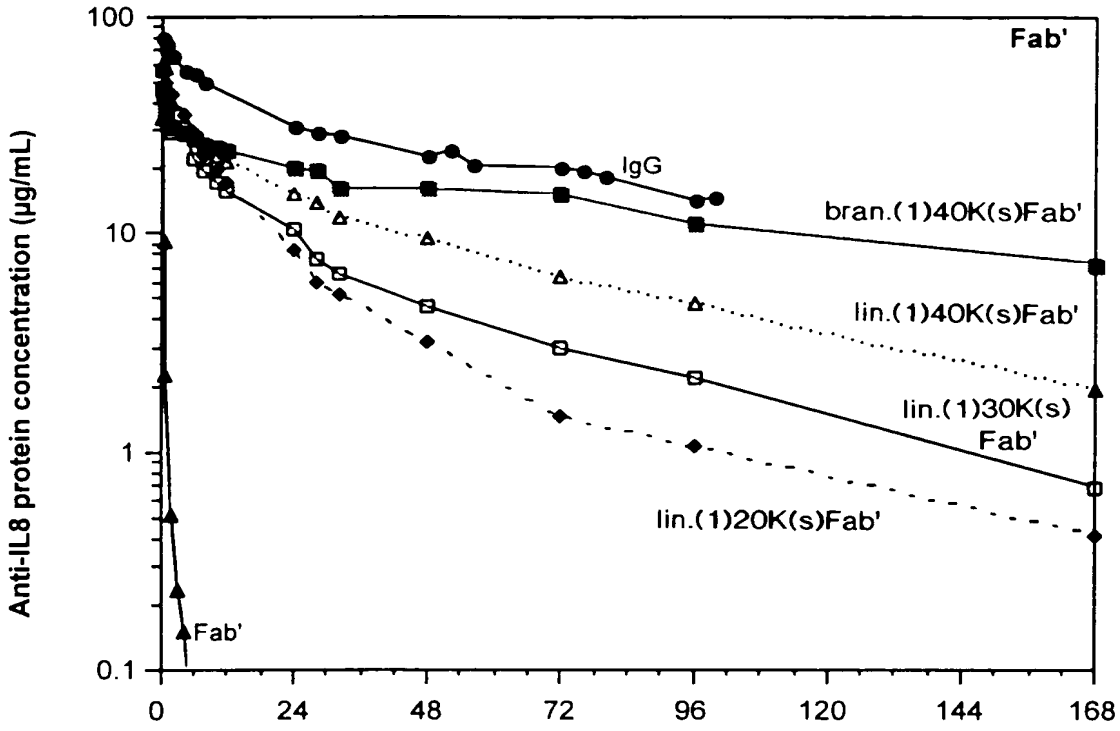


FIG. 65A

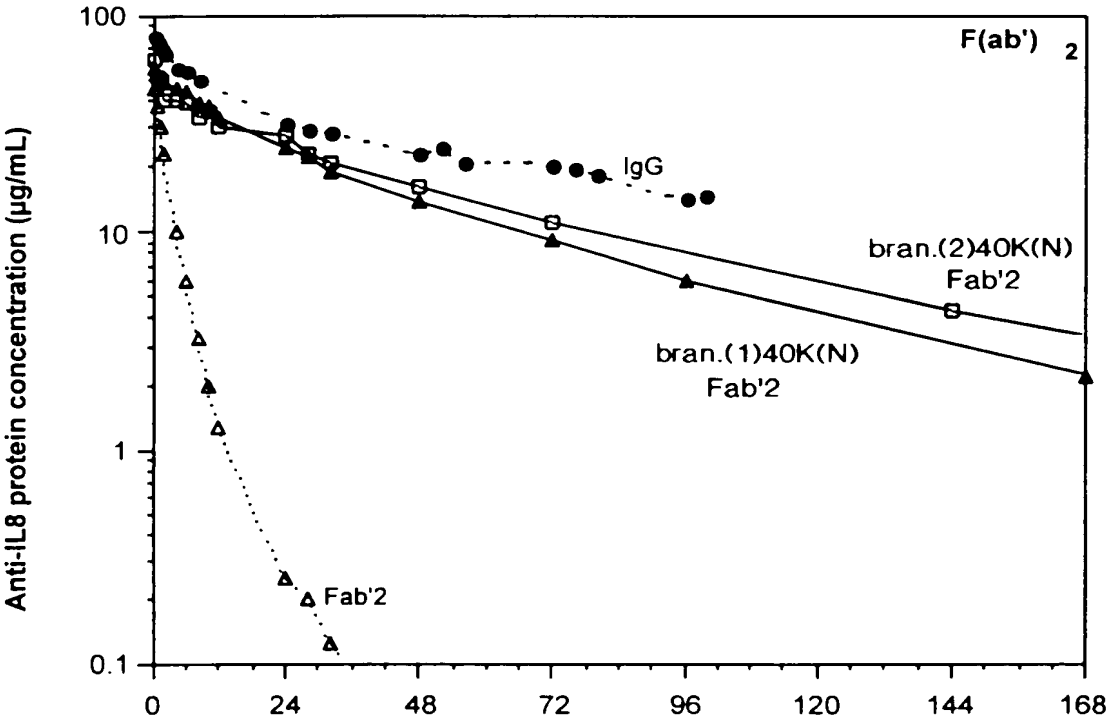


FIG. 65B

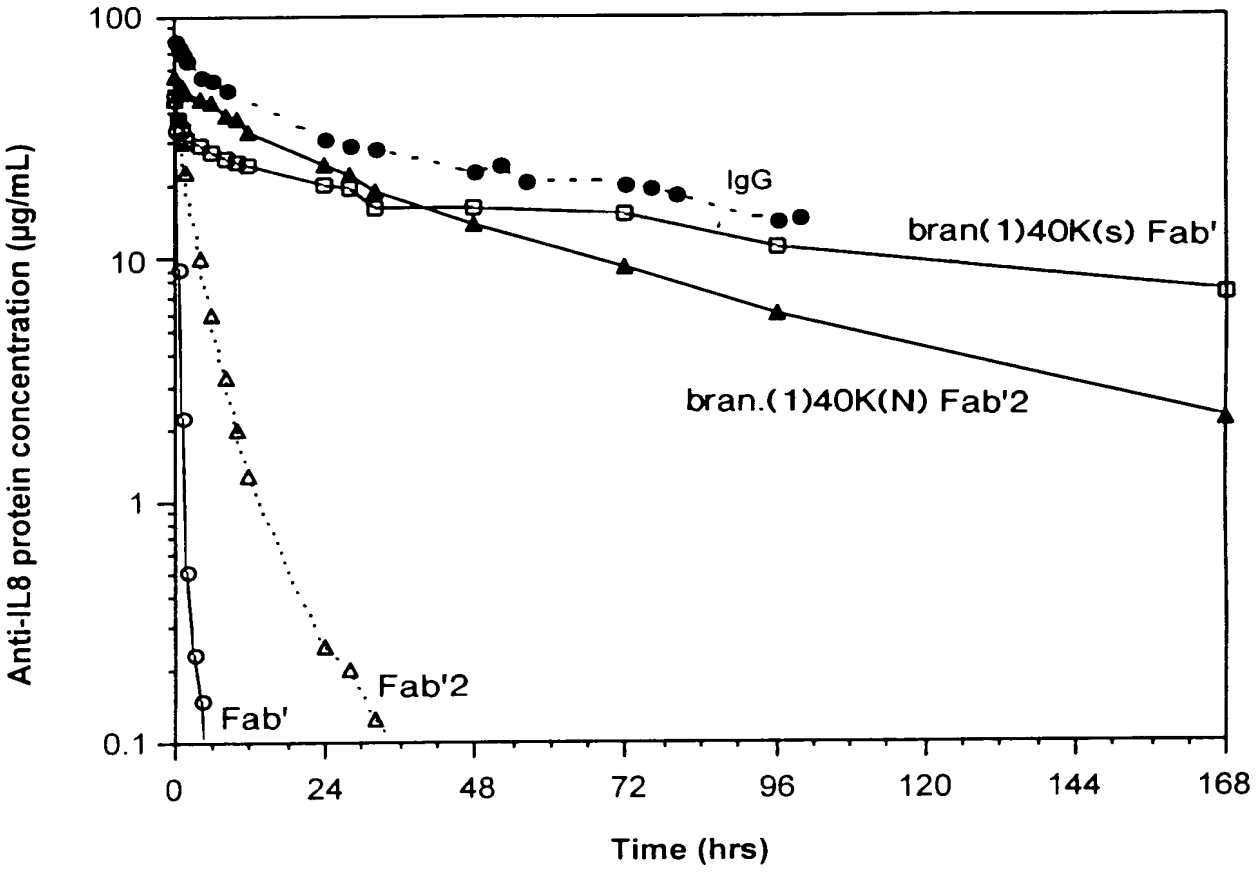


FIG. 66

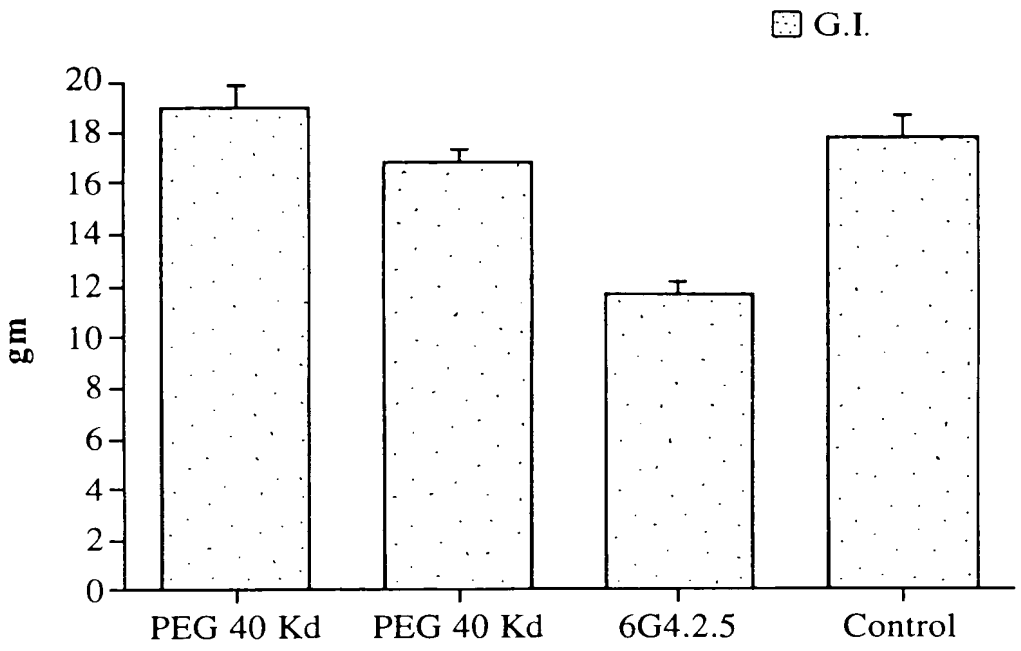


FIG. 67

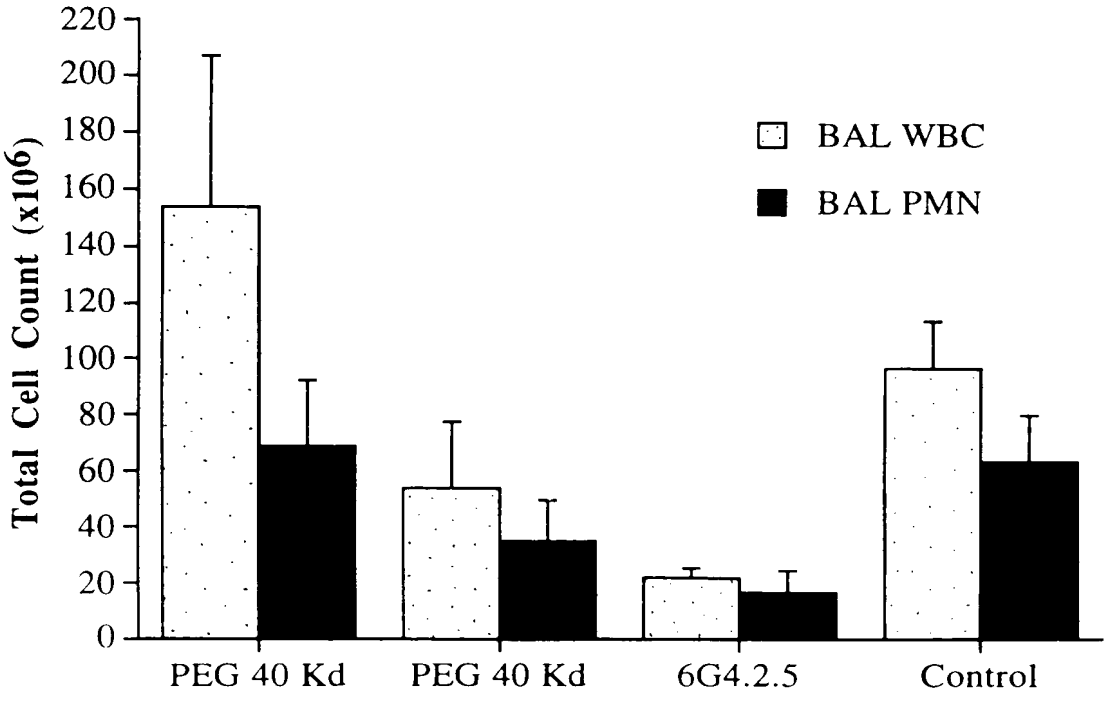


FIG. 68

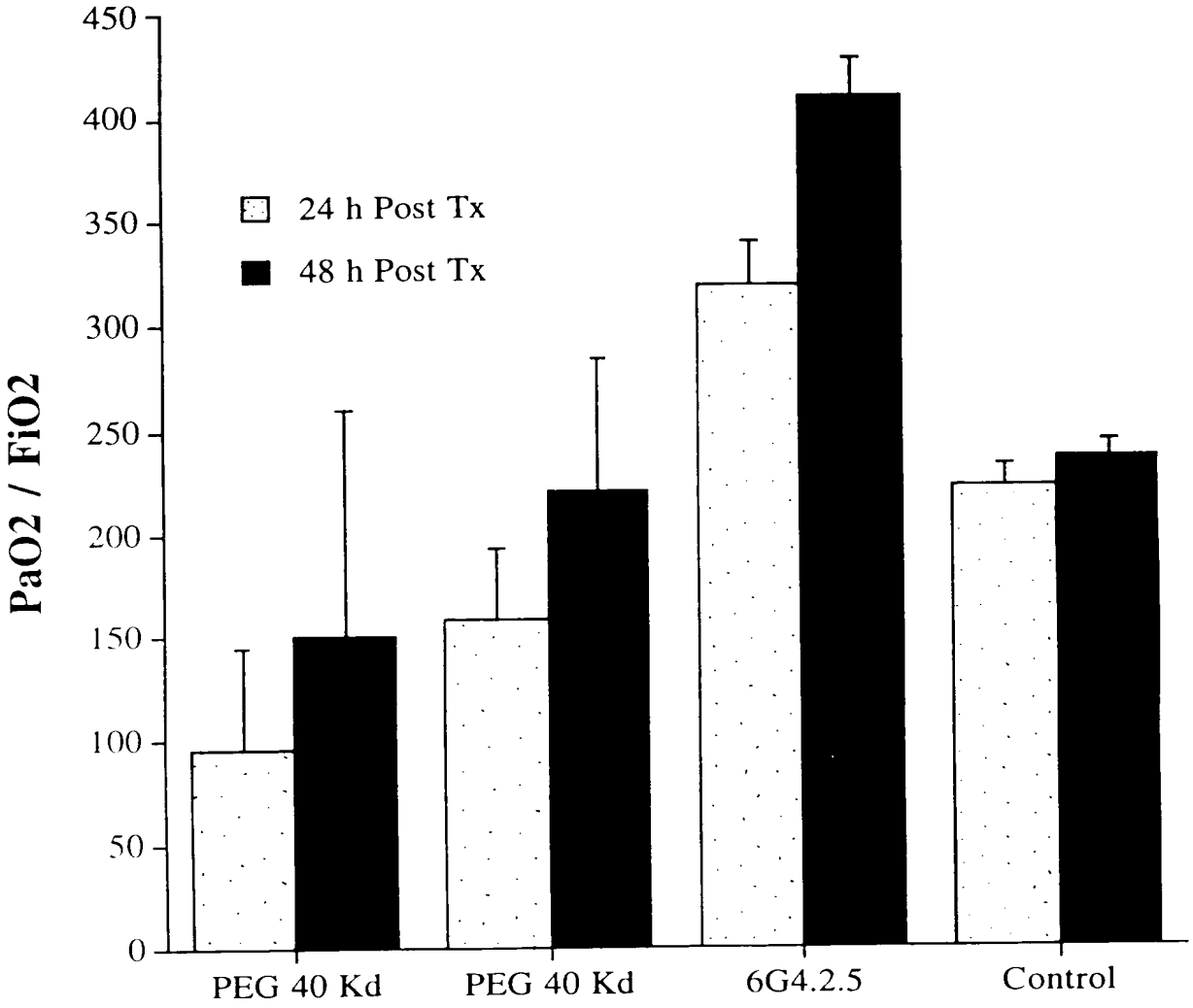


FIG. 69

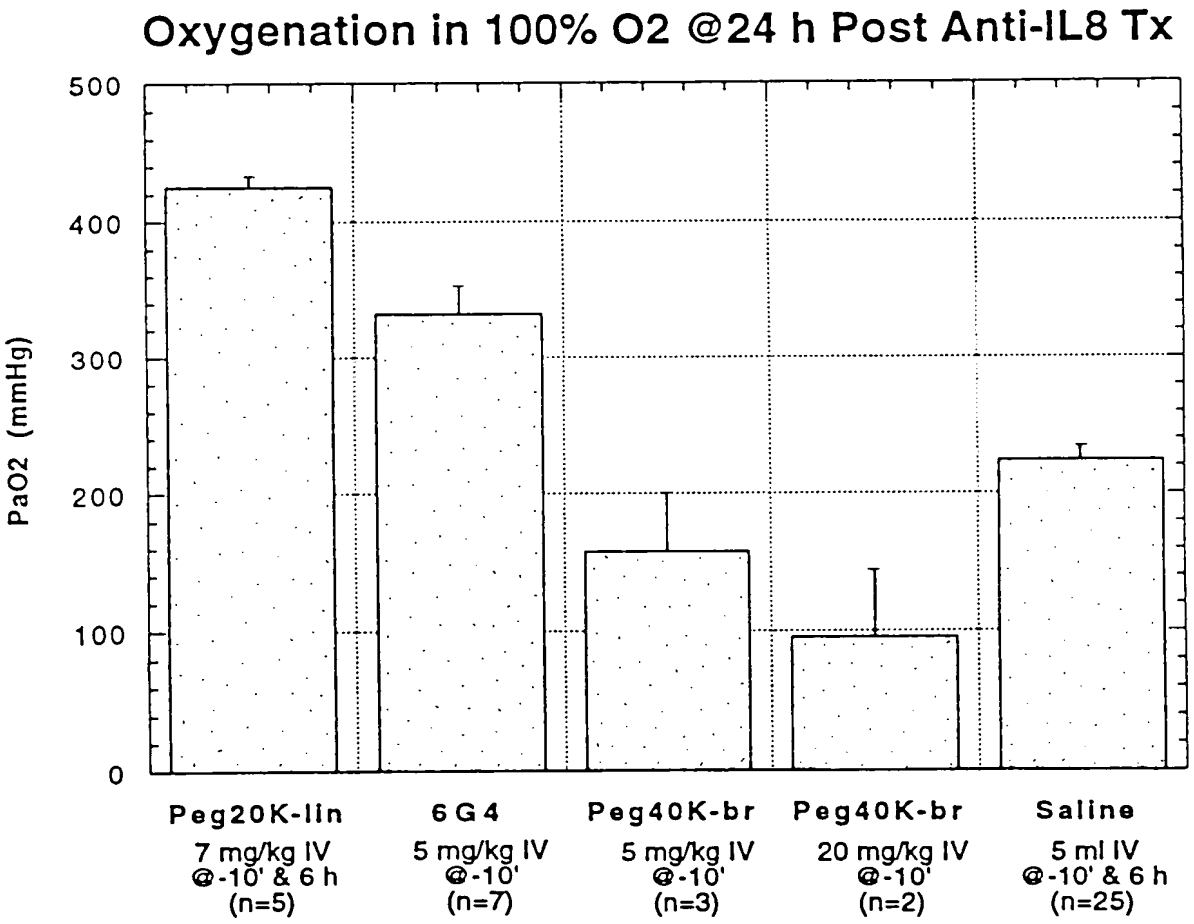


FIG. 70A

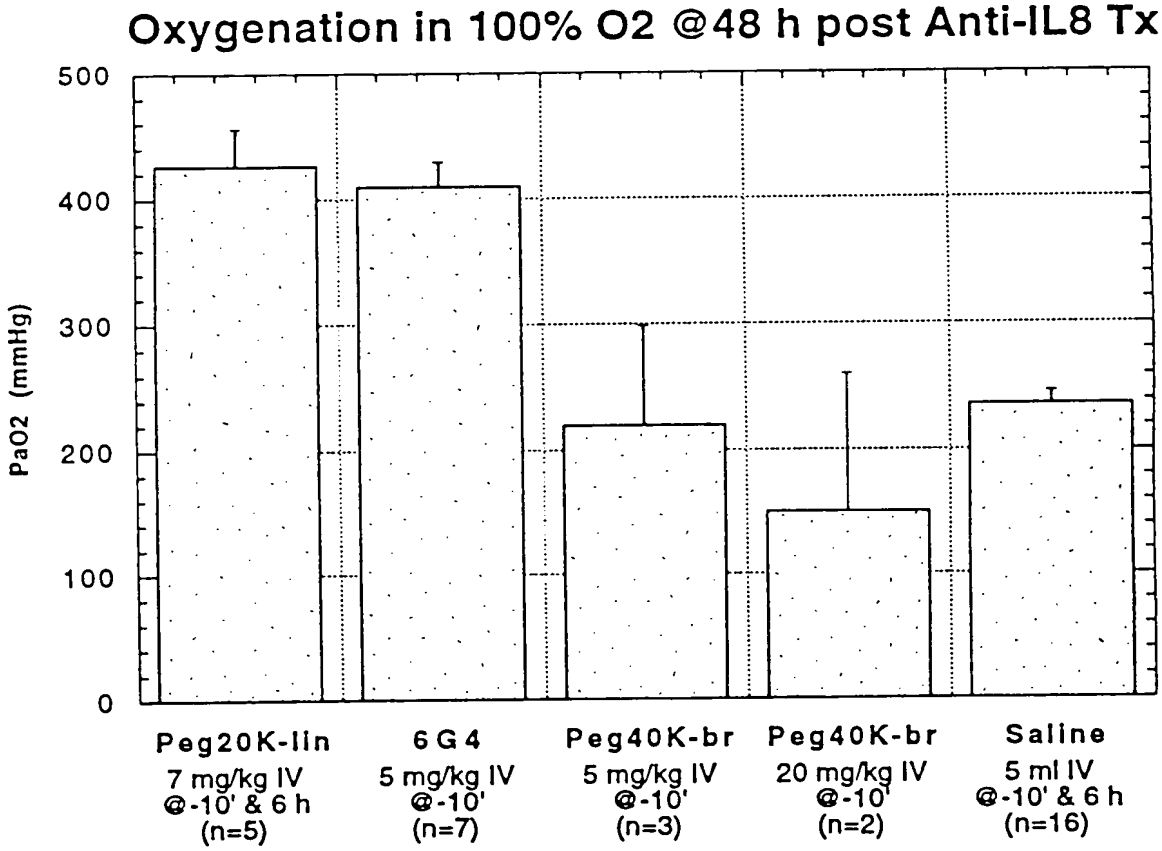


FIG. 70B

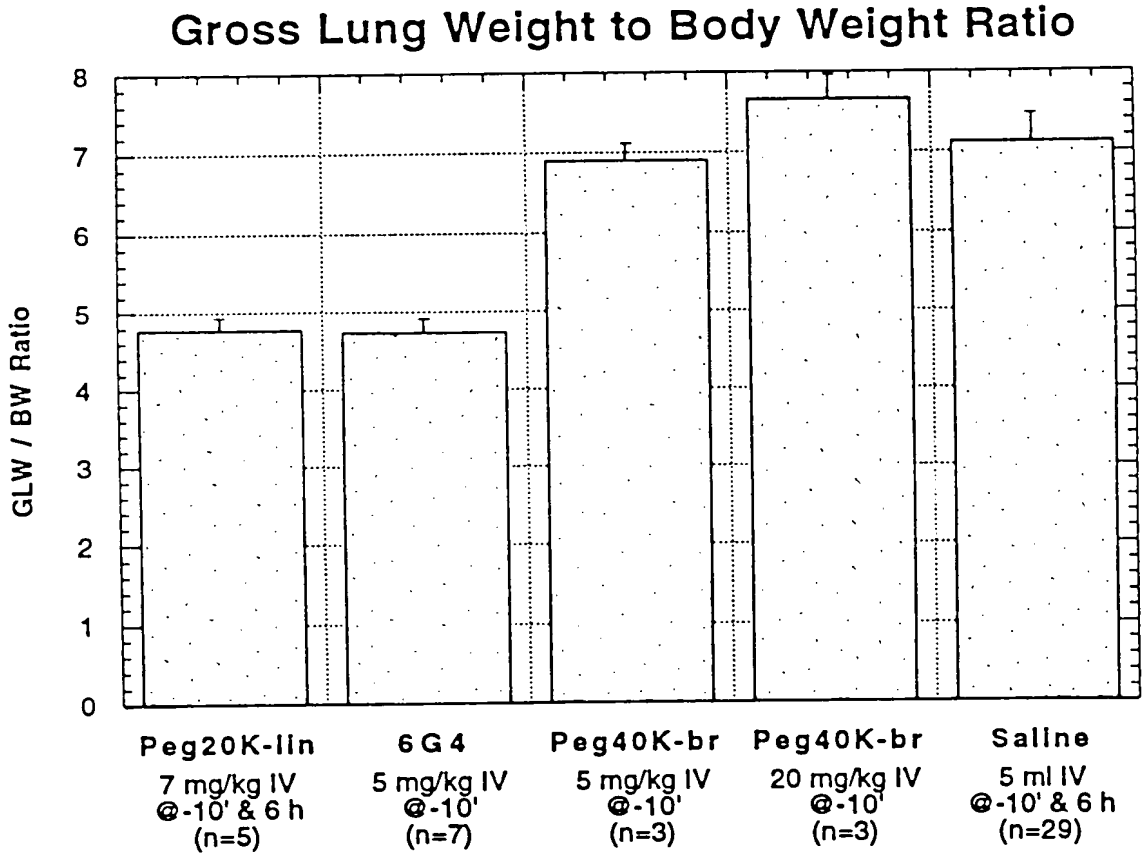


FIG. 70C

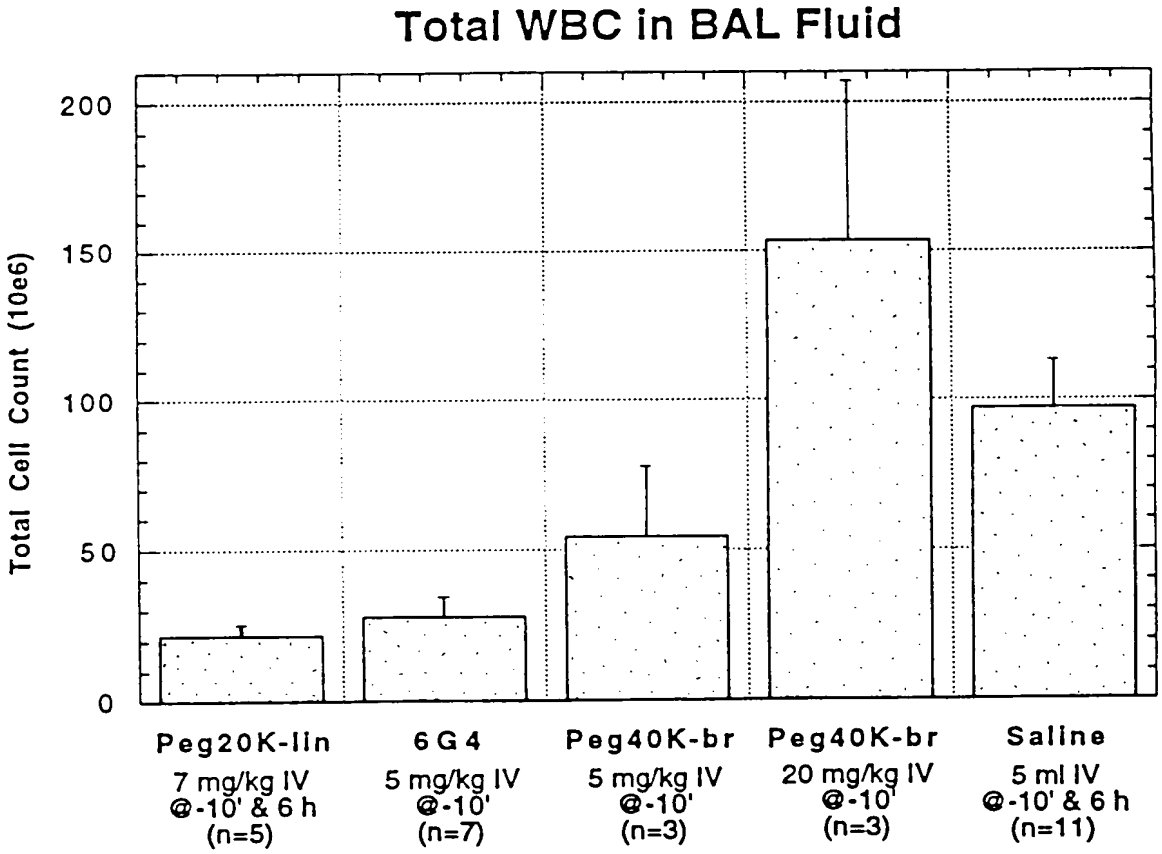


FIG. 70D

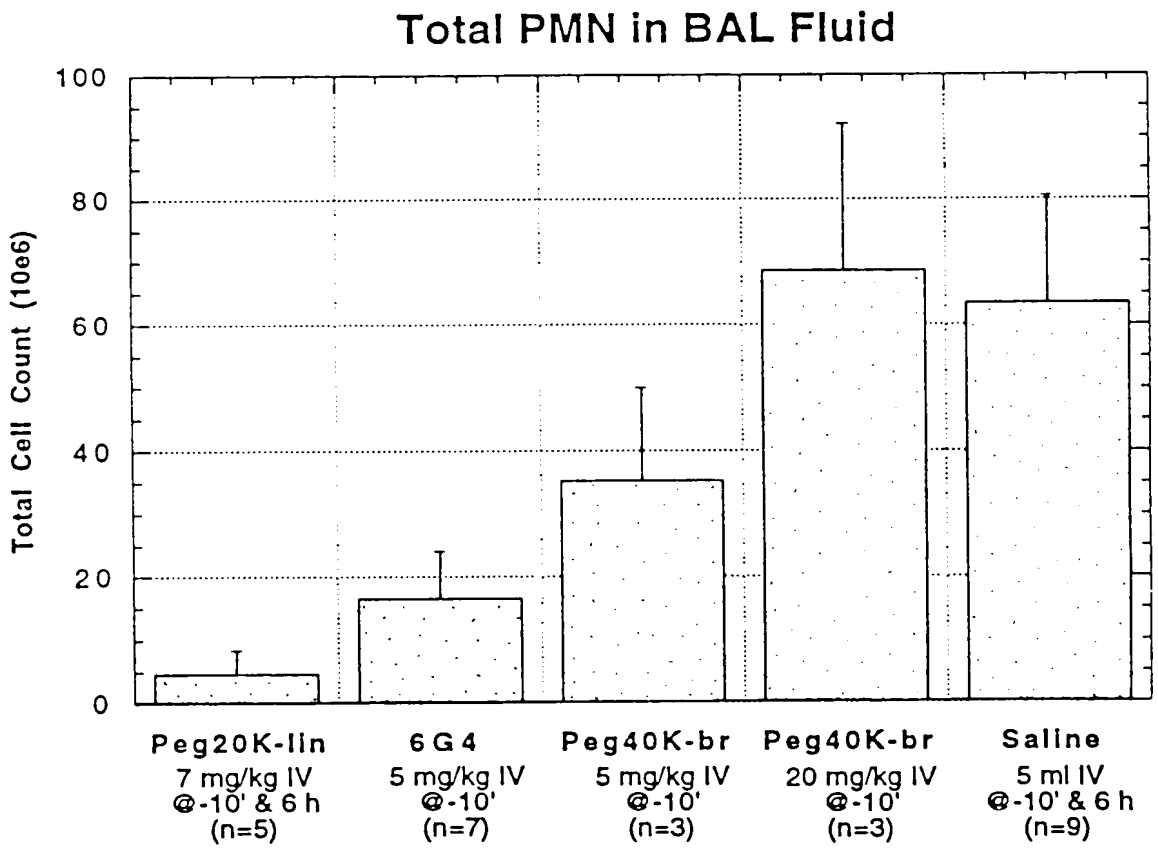
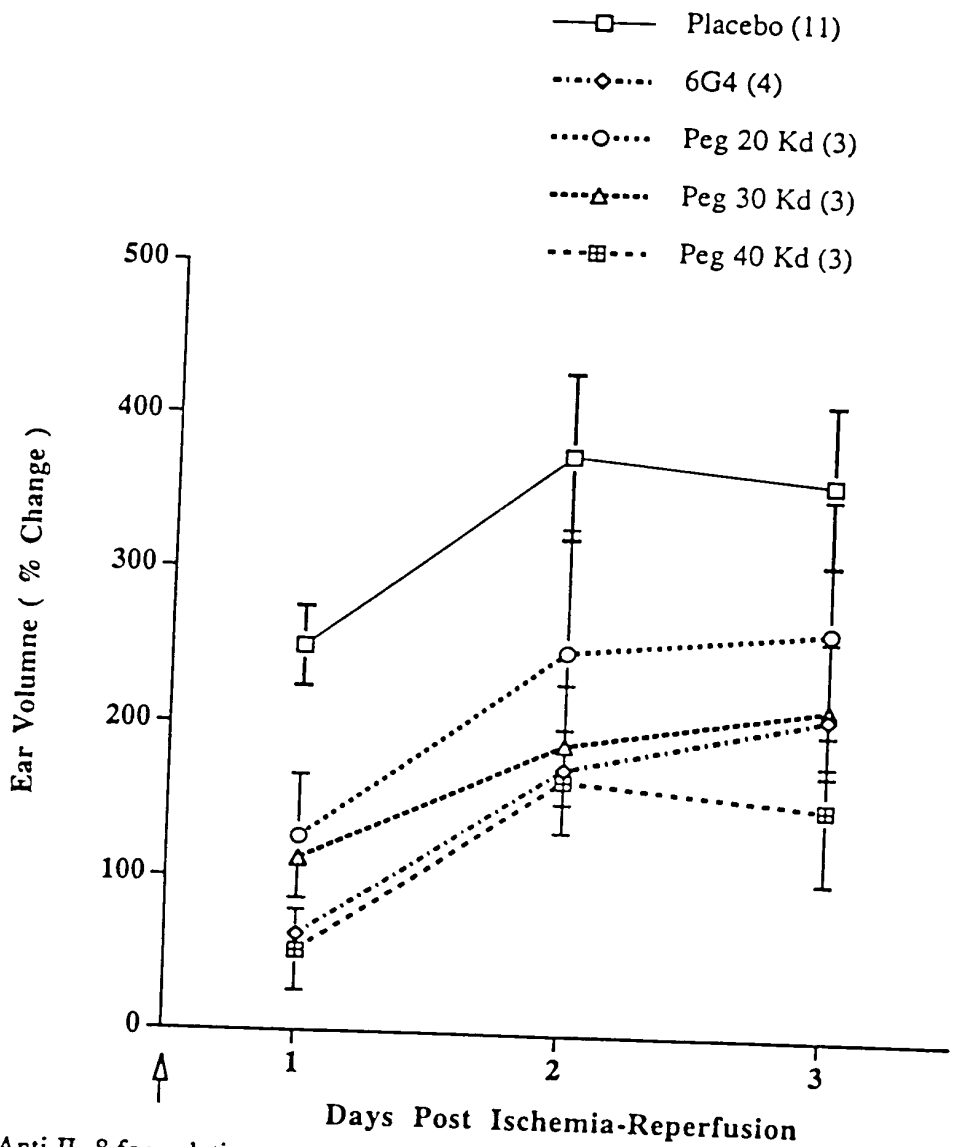

Total PMN in BAL Fluid
Total Cell Count (10e6)
100
80
60
40
20
0
Peg20K-lin
7 mg/kg IV
@-10' & 6 h
(n=5)
6G4
5 mg/kg IV
@-10'
(n=7)
Peg40K-br
5 mg/kg IV
@-10'
(n=3)
Peg40K-br
20 mg/kg IV
@-10'
(n=3)
Saline
5 ml IV
@-10' & 6 h
(n=9)

FIG. 70E

The Effect of Pegylated Anti-IL-8 in the Rabbit Ear model of Ischemia-Reperfusion Injury



Anti-IL-8 formulations : Single Dose (5 mg/kg) administered IV at time of reperfusion

FIG. 71